

09 828302

TI Protein and cDNA sequence of *Physcomitrella patens* signal transduction
stress-related proteins and uses in plants for increased tolerance to
environmental stresses

IN ***Da Costa e Silva, Oswaldo*** ; ***Bohnert, Hans J.*** ; ***Van***
*** Thielen, Nocha*** ; ***Chen, Ruoying*** ; ***Ishitani, Manabu***

PA BASF Plant Science G.m.b.H., Germany

SO PCT Int. Appl., 101 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 5

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2001077355	A2	20011018	WO 2001-US11398	20010406

TI Moss genes from ****Physcomitrella**** ****patens**** encoding
proteins involved in the synthesis of carbohydrates

IN Lerchl, Jens; Renz, Andreas; Ehrhardt, Thomas; Reindl, Andreas; Cirpus,
Petra; Bischoff, Friedrich; Frank, Markus; Freund, Annette; Duwenig, Elke;
Schmidt, Ralf-Michael; Reski, Ralf

PA Basf Plant Science G.m.b.H., Germany

SO PCT Int. Appl., 133 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2001044476	A2	20010621	WO 2000-EP12697	20001214

STIC-Biotech/ChemLib

68878

From: Collins, Cynthia
sent: Friday, June 14, 2002 6:07 PM
**:
Subject:** STIC-Biotech/ChemLib
sequence search request SN 09/828302

Please search, **both** prior art and interference, for SN 09/828302:

- 1) SEQ ID NO:9
- 2) SEQ ID NO:14

Thank You,

Cynthia Collins
Art Unit 1638
CM1, 9A12 (office) or 9E12 (mailbox)
(703) 605-1210

FD. 4/6/01 No Art
Prov 4/7/00 @ 100%
102b 4/7/99

If Contact:
Sheppard
Searcher: _____
Phone: _____; or: 305-1409
Location: _____
Date Picked Up: _____
Date Completed: 6/21/02
Searcher Prep/Review: _____
Clerical: _____
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TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
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Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

SEARCHED
JUN 17 2002
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 17:46:14 ; Search time 1689.55 seconds
(without alignments)
10752.509 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: gb_htc:*

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32 150 11.3 613 10 AW755381
33 150 11.1 635 10 BG238499
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44 147.2 10.9 560 10 BF648487
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ALIGNMENTS

RESULT 1
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DEFINITION 115F11 Mature tuber lambda ZAP mRNA linear EST 14-AUG-2001
SEQUENCE sequence.
ACCESSION BI405732
VERSION BI405732.1 GI:15185146
KEYWORDS EST.
ORGANISM Solanum tuberosum
SOURCE potato.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
ASTERIDAE; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 799)
REFERENCE Nielsen, K.L., Crookshanks, M., Emmersen, J. and Welinder, K.G.
AUTHORS
TITLE
JOURNAL
COMMENT
Unpublished (2000)
Contact: Karen G. Welinder
Institut for bioteknologi
Aalborg Universitet
Sohngaardsholmsvej 49, 9000 Aalborg, Denmark
Tel: +45 96358467
Fax: +45 98141808
Email: kgw@bio.auc.dk
Sequenced from the 5' end.
High quality sequence stop: 799
POLYA=NO.
FEATURES source
1. .799
/organism="Solanum tuberosum"
/cultivar="Field grown Kuras"
/db_xref="taxon:4113"
/clone_lib="Mature tuber lambda ZAP"
/tissue_type="Tuber"
/note="Vector: Lambda ZAP"
236 a 144 c 200 g 219 t
BASE COUNT
ORIGIN
Query Match 18.2%; score 245.6; DB 10; length 799;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	245.6	18.2	799	10	BI405732	-
2	229	17.9	414	10	BJ196973	BI405732 115F11 Ma
3	213.4	15.9	727	10	BG595786	BJ196973 BJ196973
4	205.8	15.3	577	10	BE805365	BE595786 EST494464
5	196.8	14.6	520	10	BE556233	BE805365 ss41g11.y
6	191.6	14.2	704	10	BI269796	BE556233 sp99b10.y
7	189.4	14.1	527	10	BI701028	BI269796 NF016C08I
8	186.2	13.8	497	10	BI701941	BI701028 sag54a02.
9	185.4	13.8	664	10	BF650146	BI701941 sag40b10.
10	182.8	13.6	609	10	BE330853	BF650146 NF084G11E
11	181.6	13.5	493	10	BE941416	BE330853 so86e12.y
12	177.2	13.2	478	9	BE021852	BE941416 EST420995
c	175.4	13.0	680	10	BE819869	BE021852 sm63c10.y
14	175	13.0	516	10	BI307827	BE819869 GM700002A
15	171.6	12.7	638	10	BG587548	BI307827 EST529237
16	166.8	12.4	439	9	BE057640	BG587548 EST489311
17	166.4	12.4	394	9	AI938822	BE057640 sn05b02.y

AUTHORS	van der Hoeven, R., Bezzerrides, J., Sun, H., Cho, J., Chlemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.	QY 632 cgacctggcaggctgttaaatctcgattgtacacaacccaaacctagcatgagg 691 Db 577 AGGAATGGTCAGGCATAACAAATTCTAGAGATCACAAACCTGAGCTTGATTGAGAAG 636
TITLE	Generations of ESTs from sprouting potato eyes	
JOURNAL	Unpublished (2000)	
COMMENT	Contact: Cathy Ronning The Institute for Genomic Research For clone info: Please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com Seq primer: M13F-R.	
FEATURES	Location/Qualifiers 1. .727 /organism="Solanum tuberosum" /cultivar="Kennebec" /db_xref="taxon:4113" /clone="CSTS11F23" /clone_lib="CSTS" /tissue_type="sprouting eyes from tubers" /dev_stage="12-14 weeks post harvest" /lab_host="SOLR" /note="Vector: pBluescript SK(-); Site_1: ECORI; Site_2: XHOI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers." ORGANISM	
source	RESULT 4 BE805365 LOCUS DEFINITION BE805365 SS41911.Y1 Gm-c1.061 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1061-1341 5' similar to TR:Q9SZ53 Q9SZ53 PROTEIN PHOSPHATASE 2C-LIKE PROTEIN. ; mRNA sequence. ACCESSION BE805365 VERSION BE805365.1 GI:10236477 KEYWORDS EST. SOURCE soybean. ORGANISM Glycine max Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine. 1 (bases 1 to 577) REFERENCE Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. AUTHORS Unpublished (1999) TITLE Public Soybean EST Project JOURNAL Contact: Shoemaker R/Public Soybean EST Project COMMENT Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com High quality sequence stop: 412. FEATURES Location/Qualifiers 1. .577 /organism="Glycine max" /db_xref="taxon:3847" /clone="GENOME SYSTEMS CLONE ID: Gm-c1061-1341" /clone_11b "Gm-c1061" /tissue_type="mature flowers of field grown plants" /lab_host="DH10B" /note="Vector: pBluescript II SK+; Site_1: ECORI; Site_2: XHOI; The cDNA library was constructed from mRNA isolated from mature flowers of field grown plants for the cultivar Raiden. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."	
Query Match	15.9%; Score 213.4; DB 10; Length 727; Best Local Similarity 59.0%; Pred. No. 2.7e-49; Matches 443; Conservative Matches 443; Gaps 3;	
BASE COUNT	222 a 113 c 190 g 202 t	
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Query Match	15.9%; Score 213.4; DB 10; Length 727; Best Local Similarity 59.0%; Pred. No. 2.7e-49; Matches 443; Conservative Matches 443; Gaps 3;	
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BASE COUNT	222 a 113 c 190 g 202 t	
ORIGIN		
Query		

RESULT	6	704	bp	mRNA	linear	EST 18-JUL-2001
LOCUS	BI269796	704	bp	mRNA	linear	EST 18-JUL-2001
DEFINITION	NF016C08IR1F1065 Irradiated Medicago truncatula cDNA clone					
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales; Medicago truncatula					
KEYWORDS	barrel medic.					
SOURCE	Medicago truncatula					
ORGANISM	Medicago truncatula					
REFERENCE						
AUTHORS	Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.					
TITLE	Expressed Sequence Tags from the Samuel Roberts Noble Foundation Unpublished (2001)					
JOURNAL	Plant Biology Division					
COMMENT	The Samuel Roberts Noble Foundation					
Insert Length:	704	Std Error:	0.00	RESULT	7	
Plate:	016	row:	C	column:	08	BI701028
Seq primer:	TCACACAGGAAACAGCTATGAC.	Location/Qualifiers		LOCUS	527 bp	mRNA
source	1. .704 /organism="Medicago truncatula" /db_xref="taxon:3880" /clone="NF016C08IR" /clone_lib="Irradiated" /tissue_type="seedlings" /dev_stage="seedling" /note="Vector: Lambda Zap; Seedlings were exposed either to 100 gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation. Gamma-irradiated samples were harvested at 6, 12, 24 and 48 hours after treatment. UV-irradiated samples were harvested 24 hours post-treatment. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the Uni-ZAP XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-ZAP XR vector using EXAssist helper phage and the E. coli strain XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."	DEFINITION	sag54a02.y1 Gm-c1082 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1082-28 5' similar to TR:Q9SZ53 PROTEIN PHOSPHATASE 2C-LIKE PROTEIN. ; mRNA sequence.			
base count	189 a	121 c	193 g	197 t	4 others	ACCESSION
origin						VERSION
						KEYWORDS
						SOURCE
						ORGANISM
						Glycine max
						Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids I; Fabales; Papilionoideae; Phaseoleae; Glycine.
						REFERENCE
						1 (bases 1 to 527)
						AUTHORS
						Shoemaker, R., Keim, P., Vodkin, P., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
						JOURNAL
						COMMENT
						CONTACT
						Public Soybean EST Project
						Public Soybean EST Project
						Washington University School of Medicine
						4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
						Tel: 314 286 1800
						Fax: 314 286 1810
						Email: est@watson.wustl.edu
						This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com Seq primer: -40RP from Gibco
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						/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:

into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+)) vector that has been digested with EcoRI and XbaI, and phosphorylated by Stratagene). This library was constructed in the laboratory of Dr. Paul Keim and Dr. Virginia H. Coryell at Northern Arizona

XbaI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL1R cells.^a

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 18:42:44 ; Search time 53.31 seconds
(without alignments)
6201.889 Million cell updates/sec

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Perfect score: 1346
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	120	8.9	1824	3	US-08-935-855-1	Sequence 1, Appl	
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5	99.6	7.4	2268	2	US-08-873-093-2	Sequence 2, Appl	
c	6	55.8	4.1	7218	1	US-08-232-463-14	Sequence 14, Appl
c	7	50.2	3.7	1403	3	US-09-013-881-10	Sequence 10, Appl
c	8	36.4	2.7	2750	3	US-08-617-860B-33	Sequence 33, Appl
9	35	2.6	289	4	US-09-007-005-17	Sequence 17, Appl	
10	35	2.6	289	4	US-09-244-796-17	Sequence 17, Appl	
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c	15	32	2.4	1498	1	US-08-118-469A-1	Sequence 1, Appl
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ALIGNMENTS

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; Sequence 19, Application US/08935855
; Patent No. 6066485
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; ADDRESS: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,855
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1890 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-935-855-19

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Best Local Similarity 59.5%;
Matches 235; Conservative 0; Mismatches 157; Indels 3; Gaps 1;

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/873,093
 FILING DATE: Filed Herewith
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REFERENCE/DOCKET NUMBER: 36,749
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 2:
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 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: 13177
 CLONE: THPIPLB01
 US-08-873-093-2

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 Patent No. 5670367

GENERAL INFORMATION:
 APPLICANT: DORNER, F.
 APPLICANT: SCHEIFLINGER, F.
 APPLICANT: FALKNER, F. G.
 TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:

US-08-617-860B-33 ; Sequence 33, Application US/08617860B
; Patent No. 6133506 ;
; GENERAL INFORMATION:
; APPLICANT: Tvpfer, R., Bautor, J.
; APPLICANT: Hvricle-Grandpierre, C.
; APPLICANT: Mller, A., Schulte, W.
; APPLICANT: Schell, J.
; TITLE OF INVENTION: Promoters
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steinberg, Raskin &
; STREET: 1140 Avenue of the Amer
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inc
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PatentIn Release #1.0
; CURRENT APPLICATION DATA:
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; FILING DATE: 01-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/02
; FILING DATE: 05-SEP-1994
; APPLICATION NUMBER: DE P4 329951
; FILING DATE: 04-SEP-1993
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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Cuphea lanceolata
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; CLONE: CITEg4
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Search completed: June 19, 2002, 19:49:52
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 18:43:49 ; Search time 210.22 Seconds
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ALIGNMENT

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 KW protein identification; signal transduction pathway;
 KW metabolic pathway; promoter; termination sequence;

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PR	01-JUL-1999;	99US-0142154.	PR	10-SEP-1999;	99US-0153070.
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.

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PR	19-MAY-1999;	99US-0134941.
PR	20-MAY-1999;	99US-0135124.
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PR	99US-0156458.	99US-0157865.

RESULT 9
AAH26935
ID AAH26935 standard; cDNA; 1824 BP.
XX

DR P-PSDB; ABB61123.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from *Drosophila* and for elucidating cell signalling and cell-cell interactions - PT PT

Search completed: June 19, 2002, 19:53:37
Search time: 4188 sec



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 18:11:49 ; Search time 1901.09 Seconds

(without alignments)
14816.299 Million cell updates/secTitle: US-09-828-302-9
Perfect score: 1346

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:

1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters:

3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
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ALIGNMENTS

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DEFINITION Arabidopsis thaliana AT4931860/F11C18_60 mRNA, complete cds.
ACCESSION  AY057611
VERSION   GI:16209697
KEYWORDS
SOURCE    (bases 1 to 1531)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicots; Rosidae; eurosids II; Brassicales; Arabidopsis.
REFERENCE  1
AUTHORS  Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
TITLE     Arabidopsis cDNA clones
JOURNAL  Unpublished
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description

Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Tracy,S.E., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.		Submitted (24-JUL-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA	Direct Submission	328
RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA; 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.				
The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Liu,S.X., Pham,P.K., Banh,J., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Newmann,G., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tracy,S.E., Davis,R.W., Ecker,J.R. and Theologis,A.				
Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.				
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5' UTR				
CDS				
gene				
3' UTR				
misc_difference				
BASE COUNT				
ORIGIN				
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Query 32 agaggatggaaatttatctttgtctccaaagactgacaagaacatccgaagatgttag 91 Db 155 ATATCGATGGTACATACTTAAGTTCTCCGAAAGTTATCAGAAGATGGTAG 214			RESULT 4 AF213455 LOCUS Zea mays protein phosphatase type-2C (PP2C-1) mRNA, linear PLN 03-DEC-2005 complete cds.	
Query 92 aatgccgaggtaatcgctatgttcaaggccatgcaagggtggcgatagcatggaggat 151 Db 215 ATGATAAGCTCAGATTGGTTATCGTCAAGGTGGCGCTACCATGGAAGAC 274			DEFINITION AF213455 ACCESSION AF213455 VERSION AF213455.1 GI:12003989 KEYWORDS SOURCE Zea mays ORGANISM Zea mays	
Query 152 gcacacaaagcttatcttaaacgttggataagaacacgtcaacatcaatatttggcatcttt 211				

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>

Series: IRAL Plate: 24 Row: 9 Column: 23.

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CDS	<p>BASE COUNT ORIGIN</p> <pre> <1..1012 /codon_start=2 /product="Similar to protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform" /protein_id="AAH07361.1" /db_xref="GI:13938440" /translation="ARGFSNSNERTEAGQVGEPIPTGEAGPSCSSASDKLPRVAKS KFFEDSEDESAEEEEEEDSEEECSEEEDGYSSSEAENEEDDTEEEAEDDEEEFEM MWPMEGKEEFGSDSGTTAVVALIRKGKOLJYANAGDSRCVVSSEAGKALDMSYDHKFED EVELARIKNAGKVTMDGRVNGLNLSRAIGDFYKRKNKNLPPPEQMISALPDIKVLT LTDIDHEFMVIALCDGIVNWMSQEVVDFIQSISKISQRDENGEILRLSSIVEELLDQCCLAP DTSGDGTGCDNMTCITIFCKPRNTAELQPESGKRKLEEVLSSTEGAEEENGNSDKKKAK RD" </pre> <p>373 a 333 c 417 g 311 t</p>
FEATURES source	<p>Query Match 9.5%; Score 127.8; DB 9; Length 1434; Best Local Similarity 59.5%; Pred. No. 1e-25; Matches 235; Conservative 0; Mismatches 157; Indels 3; Gaps 1;</p>
FEATURES source	<p>Qy 550 tgggagtactgcagggtggctgtgattcggtggcaataaaactgttcgtcgcaaaacgctgg 609 Db 352 TGGTACAACAGCCGGTGGGCCCTGATAACGAGGCAACTGTAGGCCAACGGCAG 411</p>
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FEATURES source	<p>Qy 787 tgcacctgttgcacccgtgacaaaggcaagtgtacgtggccgtgttgtcgaaatgg 846 Db 592 AAACAAGAACCTGCACCTGAGGAACAGATGATTTAGCCCTTCTCTGACATCAAAGGTGC 651</p>
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FEATURES source	<p>AUTHORS Pohl, J.D. and Hanke, M.D. TITLE Nucleic acid encoding a human protein phosphatase . JOURNAL Patent: EP 0874052-A 3 28-OCT-1998; FEATURES BIOPH BIOTECH ENTR PHARM GMBH (DE) source Location/Qualifiers 1..1641 /organism="unidentified" /db_xref="taxon:32644" /tissue_type="HUMAN PLACENTA" BASE COUNT 462 a ORIGIN 372 c 500 g 307 t</p>
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FEATURES source	<p>RESULT 9 HSY13936 LOCUS HSY13936 1932 bp mRNA linear PRI 04-AUG-1997 DEFINITION Homo sapiens mRNA for protein phosphatase 2C gamma. ACCESSION Y13936 VERSION Y13936.1 GI:2315201 KEYWORDS protein phosphatase 2C gamma. SOURCE human. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 1932) AUTHORS Travis, S.M. TITLE Direct Submission JOURNAL Submitted (19-JUN-1997) Travis S.M., Internal Medicine, University of Iowa, 500 EMRB, Iowa City IA 52242 USA MEDLINE 97420453 FEATURES source 1..1932 /organism="Homo sapiens" /db_xref="taxon:9606" /tissue_type="Skeletal muscle" 25..1665 CDS</p>

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BASE COUNT 871 a 460 c 506 g 673 t ORIGIN

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Best Local Similarity 55.1%; Pred. No. 9.1e-25;
Matches 288; Conservative 0; Mismatches 229; Indels 6; Gaps 2;

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QY 1024 aggatgtgataacatgaggcatcattatgtccaaaccaaaggca 1066
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ACCESSION L34881
VERSION L34881.1 GI: 609655
KEYWORDS protein phosphatase 2C.
SOURCE Schizosaccharomyces pombe (strain 972) DNA.
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomyctaceae;
Schizosaccharomyces.
REFERENCE 1 (bases 1 to 1920)
AUTHORS Shiozaki, K. and Russell, P.
TITLE Counteractive roles of protein phosphatase 2C (PP2C) and a MAP kinase kinase homolog in the osmoregulation of fission yeast
JOURNAL EMBO J. 14 (3), 492-502 (1995)
MEDLINE 95163582
FEATURES Location/Qualifiers
source 1. 1920
/organism="Schizosaccharomyces pombe"
/strain="972"
/db_xref="taxon:4896"
CDS 595. .1707

Search completed: June 19, 2002, 19:48:36
Job time: 5807 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 19, 2002, 08:43:46 ; Search time 28.56 Seconds
 (without alignments)
 2138.208 Million cell updates/sec

Title: US-09-828-302-14

Perfect score: 1836
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Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 5622222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0*

Maximum Match 100*

Listing first 45 summaries

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- 3: sp_fungi:*
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- 8: sp_organelle:*
- 9: sp_phage:*
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- 11: sp_rabbit:*
- 12: sp_virus:*
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- 15: sp_rvirus:*
- 16: sp_bacteriaph:*
- 17: sp_archeap:*

SPTREMBL_19:*

- 1: sp_archaea:*
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ALIGNMENTS

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AC	Q9FQY2;
DT	01-MAR-2001 (TREMBLrel. 16, Created)
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	PROTEIN PHOSPHATASE TYPE-2C.
GN	PP2C-1.
OS	Zea mays (Maize).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC	Panicoideae; Andropogoneae; Zea.
NCBI_TaxID	4577;
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RN	SEQUENCE FROM N.A.
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RA	Broz A.K., Thelen J.J., Miernyk J.A., Muszynski M.G., Randall D.D.;
RT	"ZmpP2, a novel type-2C protein phosphatase from maize.";
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF213455; AAG43835.1; -.
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RA	Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Eckert J.R., Theologis A.;	Full Length cDNA of gene F27C12.1/At2g25070 (GI:4559345).";	RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Hernandez J.R., Houck J., Heiman T.J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McPherson D., Merkulov G., Milashina N.V., Mobarry C., Morris J., Moshefi A., Mount S.M., Moy M., Murphy B., Murzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Purif V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner E., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;	RA
DR	InterPro; IPR000222; PP2C.	DR	Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Hernandez J.R., Houck J., Heiman T.J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McPherson D., Merkulov G., Milashina N.V., Mobarry C., Morris J., Moshefi A., Mount S.M., Moy M., Murphy B., Murzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Purif V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner E., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;	RA	
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DR	PROSITE; PS01032; PP2C; 1.	DR	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.	RL	
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		DR	FlyBase; FBgn0033021; CG10417.	DR	
		DR	InterPro; IPR000222; PP2C.	DR	
		DR	InterPro; IPR001932; PP2C_domain.	DR	
		DR	Pfam; PF00481; PP2C; 2.	DR	
		DR	SMART; SM00332; PP2CC; 1.	DR	
		DR	PROSITE; PS01032; PP2C; 1.	DR	
		DR	FlyBase; FBgn0033021; CG10417.	DR	
		DR	InterPro; IPR000222; PP2C.	DR	
		DR	InterPro; IPR001932; PP2C_domain.	DR	
		DR	Pfam; PF00481; PP2C; 2.	DR	
		DR	SMART; SM00332; PP2CC; 1.	DR	
		DR	PROSITE; PS01032; PP2C; 1.	DR	
		DR	FlyBase; FBgn0033021; CG10417.	DR	
		DR	InterPro; IPR000222; PP2C.	DR	
		DR	InterPro; IPR001932; PP2C_domain.	DR	
		DR	Pfam; PF00481; PP2C; 2.	DR	
		DR	SMART; SM00332; PP2CC; 1.	DR	
		DR	PROSITE; PS01032; PP2C; 1.	DR	
		DR	FlyBase; FBgn0033021; CG10417.	DR	
		DR	InterPro; IPR000222; PP2C.	DR	
		DR	InterPro; IPR001932; PP2C_domain.	DR	
		DR	Pfam; PF00481; PP2C; 2.	DR	
		DR	SMART; SM00332; PP2CC; 1.	DR	
		DR	PROSITE; PS01032; PP2C; 1.	DR	
		DR	FlyBase; FBgn0033021; CG10417.	DR	
		DR	InterPro; IPR000222; PP2C.	DR	
		DR	InterPro; IPR001932; PP2C_domain.	DR	
		DR	Pfam; PF00481; PP2C; 2.	DR	
		DR	SMART; SM00332; PP2CC; 1.	DR	
		DR	PROSITE; PS01032; PP2C; 1.	DR	
		DR	FlyBase; FBgn0033021; CG10417.	DR	
		DR	InterPro; IPR000222; PP2C.	DR	
		DR	InterPro; IPR001932; PP2C_domain.	DR	
		DR	Pfam; PF00481; PP2C; 2.	DR	
		DR	SMART; SM00332; PP2CC; 1.	DR	
		DR	PROSITE; PS01032; PP2C; 1.	DR	

QY	135	- - - - - AREDDE- - - - -	SDSYSAYVLTESNDSNLAT-----	158	RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weissenbach J., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhou X., Zhu S., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of <i>Drosophila melanogaster</i> ," <i>Science</i> 287: 2185-2195 (2000).
Db	239	SNTTSINDLSTKNAALKDDSVNDQNNEGNSNGTDFKHTLVSSNNKKLFATGSNDMTELNQS	298	RA	HSSP; P35813; 1A6Q.	
QY	159	KKHKY - - - - -	SDFQ - - - - -	167	RA	FlyBase; FBgn0035425; CG17746.
Db	299	SKNEFTNSSTSKEFERNINSSQDDEFTDDADYEENDNVKS PDTSSAESSDCTENDDDGD	358	RA	InterPro; IPR0019322; PP2C.	
QY	168	- - - - - GPIYGSTAVVALIRGNKLFVANAGDSRCIM	197	DR	InterPro; IPR0019322; PP2C_domain.	
Db	359	EDGNEDSDEEETDEDQMANDNF CANMIEEPGKDSGGCTAVCVCLLQGRDLVYANAGDSRCVI	418	DR	Pfam; PF00481; PP2C.	
QY	198	SRRGEAVNLSTDHKPNLEHERKRIESAGGFVH - GGRVNGSLNITRAIGDMEMFKGRPDLP	256	DR	SMART; SM000332; PP2CC.	
Db	419	SRSQOAIEMSIDHKPEDDEASRIKAGGRVTLDGRVNGGLNLSRALGDHAYKTNTLPA	478	DR	SMART; SM000331; PP2C_SIG; 1.	
QY	257	DKQVVTCCPDVVEDLGP GDEFIVLACDG IWDMYMSQAVDFVKSRUPTTKTLSSLCEEI	316	DR	PROSITE; PS01032; PP2C; 1.	
Db	479	EEQMISALPDIKLIITPEDEFMVLA CDG IWDMYSSEEVEFVR CRLLKD NKKLSTICEEL	538	SQ	SEQUENCE 371 AA; 41009 MW; EA5A512772C2E36D CRC64;	
QY	317	LDYCLSPTTR-QQE GDPNMSLIIIVQPK-----QSGVVAASSSTD	353	Query	Match 30.4%; Score 558.5; DB 5; Length 371;	
Db	539	FDNCLAPNTMGDTGCDNMTAVIVQFKKLQELQSTIPPNOTED	582	Best Local Similarity 37.6%; Pred. No. 5.8e-37;		
RESULT	5	PRELIMINARY;	PRT;	Mismatches 50; Indels 59; Gaps 5;		
Q9VZS1	ID	Q9VZS1; PRELIMINARY;	PRT;	371 AA.		
AC	01-MAY-2000	(TREMBLrel. 13, Created)	QY	1 MGIVLCSPKTDKTSSEDDENAEELRYGLSAMQGWRDMSMEDAHKAILNVDKNTSTSIFGIFDG 60		
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)	Db	1 MGQTSEPVTAKE SAYCQNAAYRVGSSCMQGWRINMEDSHTHILSLPDDPGAAFFAVYDG 60		
DT	01-OCT-2001	(TREMBLrel. 18, Last annotation update)	QY	61 HGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSLFLRMDDEMKGASGWKELQSLEETS 120		
DE	CG17746 PROTEIN.	Db	61 HGGATVAQYAGKHLHKYVLKRPEY-NDNIEQALQQGFLDTDYYM----- 103			
GN	CG17746.	QY	121 SQLDKLGNGNSSSNAREDDSDSYAVLTESNDSNLATKKHHKYSDFQGPYIYGSTAVVALI 180			
OS	Drosophila melanogaster (Fruit fly).	Db	104 -----LRNKTCDQ----- MAGSTAVVVL 123			
OC	Eukaryota; Arthropoda; Tracheata; Hexapoda; Insecta;	QY	181 RGNKLKVANAGDSRCIMS RGEAVNLSIDHKPNLHEKRIE SAGGFVH GRVNGSLNLT 240			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	Db	124 KDNKLYCANAGDSRATACVNGQLEVLSDHKPNNEAESKR1IQGGWWEFRVNGNLALS 183			
OC	Ephydriidea; Drosophilidae; Drosophila.	QY	241 RAIGDMEFKGRPDLPDKQVVTCCPDPVVEDLGP GDEFIVLACDG IWDMYMSQAVVDFVK 300			
OX	NCBI_TaxID=7227;	Db	184 RALGDYVFK-HENKKPEDQIVTAFDPVETRKIMDWFIVLACDG IWDMMSNAEVLEFCR 242			
RN	[1]	SEQUENCE FROM N.A.	RESULT	6		
RP	SEQUENCE FROM BERKELEY;	Q9WQ00	PRELIMINARY;			
RC	REMLINE=20196006; PubMed=10731132;	ID	PRT; 352 AA.			
RX	RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champé M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra T., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin R.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milashina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy L., Muzzen D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Purvi V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,	OS	Drosophila melanogaster (Fruit fly).		
RA	SEQUENCE FROM N.A.	OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
RA	STRAIN=BERKELEY;	OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
RA	MEDLINE=20196006; PubMed=10731132;	OC	Ephydriidea; Drosophilidae; Drosophila.			
RA	[1]	SEQUENCE FROM N.A.	NCBI_TaxID=7227;	Drosophila melanogaster (Fruit fly).		
RA	SEQUENCE FROM N.A.	RN	SEQUENCE FROM N.A.			
RA	STRAIN=BERKELEY;	RP	SEQUENCE FROM N.A.			
RA	MEDLINE=20196006; PubMed=10731132;	RC	SEQUENCE FROM N.A.			
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champé M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelsson C.R., Miklos G.L.G.,	RX	SEQUENCE FROM N.A.			

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Query Match      29.9%; Score 549; DB 5; Length 367;
Best Local Similarity 35.0%; Pred. No. 3.3e-36;
Matches 126; Conservative 61; Mismatches 103; Indels 70; Gaps 7;

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Gencore version 4.5
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OM protein - protein search, using sw model

Run on: June 19, 2002, 08:44:06 ; Search time 13.42 Seconds
(without alignments)
1018.480 Million cell updates/sec

Title: US-09-828-302-14
Perfect score: 1836
Sequence: 1 MGIYLCSPKTDKTSEDDENA.....MSIIIVQPKQSGVAAASSSTD 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	64.3	35.0	546	1	P2CG_HUMAN	015355 homo sapien	
2	641.5	34.9	542	1	P2CG_MOUSE	Q61074 mus musculu	
3	641	34.9	543	1	P2CG_BOVIN	P79126 bos taurus	
4	635	34.6	370	1	P2C2_SCHPO	Q09172 schizosacch	
5	616.5	33.6	300	1	P2C_PART	P49444 paramecium	
6	608.5	33.1	414	1	P2C3_SCHPO	Q09173 schizosacch	
7	606	33.0	356	1	P2C2_CAEEL	P49596 caenorhabdi	
8	555.5	30.3	491	1	P2C1_CAEEL	P49595 caenorhabdi	
9	554.5	30.2	464	1	P2C2_YEAST	P39966 saccharomy	
10	539	29.4	390	1	P2CB_MOUSE	P36993 mus musculu	
11	538	29.3	479	1	P2CB_HUMAN	Q75688 homo sapien	
12	537	29.2	387	1	P2CB_BOVIN	Q62830 bos taurus	
13	537	29.2	468	1	P2C3_YEAST	P34221 saccharomy	
14	534	29.1	390	1	P2CB_RAT	P35815 rattus norv	
15	522	28.4	382	1	P2CA_RAT	P20650 rattus norv	
16	521	28.4	382	1	P2CA_BOVIN	Q62829 bos taurus	
17	520	28.3	382	1	P2CA_RABBIT	P35814 oryctolagus	
18	519	28.3	382	1	P2CA_MOUSE	P49443 mus musculu	
19	517	28.2	382	1	P2CA_HUMAN	P35813 homo sapien	
20	398.5	21.7	393	1	YBX5_YEAST	P38089 saccharomy	
21	357.5	19.5	423	1	P2C2_ARATH	P04719 arabidopsis	
22	354	19.3	434	1	P2C1_ARATH	P49597 arabidopsis	
23	350.5	19.1	388	1	P2C3_ARATH	P49599 arabidopsis	
24	343.5	18.7	347	1	P2C1_SCHPO	P40371 schizosacch	
25	341.5	18.6	281	1	P2C1_YEAST	P35182 saccharomy	
26	334	18.2	399	1	P2C4_ARATH	P49598 arabidopsis	
27	326	17.8	406	1	P2C_LEITCH	P36982 leishmania	
28	298.5	16.3	454	1	P2CH_HUMAN	P49593 homo sapien	
29	253	13.8	2493	1	CYAA_UTSMA	P49606 ustilago ma	
30	247	13.5	1839	1	CYAA_SACKL	P23466 saccharomy	
31	242.5	13.2	449	1	FEM2_CAEEL	P49594 caenorhabdi	
32	242.5	13.2	2026	1	CYAA_YEAST	P08678 saccharomy	
33	239	13.0	605	1	P2CD_HUMAN	O15297 homo sapien	

34 235 12.8 598 1 P2CD_MOUSE
35 223 12.1 530 1 PDP2_RAT
36 222.5 12.1 538 1 PDP1_RAT
37 218.5 11.9 538 1 PDP1_BOVIN
38 218 11.9 2300 1 CYAA_NEUCR
39 217.5 11.8 538 1 PDP1_HUMAN
40 205.5 11.2 2145 1 CYAA_PODAN
41 203.5 11.1 529 1 PDP2_HUMAN
42 190 10.3 581 1 KAPP_ARATH
43 172 9.4 1692 1 CYAA_SCHPO
44 158 8.6 383 1 P2C4_SCHPO
45 156.5 8.5 504 1 TAB1_HUMAN

Q9qz67 mus musculu
O88484 rattus norv
O88483 rattus norv
P35816 bos taurus
Q01631 neurospora
Q9P011 homo sapien
Q01513 podospora a
Q9P219 homo sapien
P46014 arabidopsis
P14605 schizosacch
O14156 schizosacch
Q15750 homo sapien

ALIGNMENTS

RESULT 1
P2CG_HUMAN STANDARD; PRT; 546 AA.
ID P2CG_HUMAN
AC O15355;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein phosphatase 2C gamma isoform (EC 3.1.3.16) (PP2C-gamma)
DE (Protein phosphatase magnesium-dependent 1 gamma) (Protein phosphatase LC).
DE PPM1G OR PPM1C.
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RA NCBI_TAXID=9606;
RX MEDLINE=97420453; PubMed=9276438;
RA Travis S.M.; Welsh M.J.;
RT "PP2C gamma: a human protein phosphatase with a unique acidic domain."
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Straussberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
CC -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
CC -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (Potential).
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED. MOST ABUNDANT IN TESTIS,
CC SKELETAL MUSCLE, AND HEART.
CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Straussberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
CC -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
CC -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (Potential).
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED. MOST ABUNDANT IN TESTIS,
CC SKELETAL MUSCLE, AND HEART.
CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
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CC or send an email to license@isb-sib.ch).
CC EMBL; Y13936; CAA74245.1; -.
DR EMBL; BC000057; AAH00057.1; -.
DR HSSP; P35813; 1A6Q.
DR MIM; 605119; -.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C_domain.
DR Pfam; PF00481; PP2C; 2.
DR SMART; SM00331; PP2C_SIG; 1.
DR SMART; SM00332; PP2CC; 1.
DR PROSITE; PS01032; PP2C; 1.
DR Hydrolase; Magnesium; Multigene family.
FT METAL 40 40 MANGANESE 1 (BY SIMILARITY).

FT METAL 41 41 MANGANESE 1 (BY SIMILARITY).
 FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 441 441 MANGANESE 2 (BY SIMILARITY).
 FT METAL 496 496 MANGANESE 2 (BY SIMILARITY).
 FT DOMAIN 258 326 ASP/GLU-RICH ACIDIC.
 FT DOMAIN 266 272 POLY-GLU.
 FT DOMAIN 306 311 POLY-GLU.
 FT DOMAIN 539 544 POLY-LYS.
 SQ SEQUENCE 546 AA; 59271 MW; 084C16F825233D9 CRC64;

Query Match 35.0%; Score 643; DB 1; Length 546;
 Best Local Similarity 32.7%; Pred. No. 2.4e-42;
 Matches 165; Conservative 60; Mismatches 112; Indels 168; Gaps 9;

Qy 1 MGIYLCSPTKTDKTSEDDENA---ELRYGLSAMQGWRDMSMEDAHKA
 LNVDKNTSTSIFGI 57
 Db 1 MGAYLQSOPNTVKCGDGVGAPRLPLPYGFSAAMQGWRVSMEDAHNC
 IPFLD-SETAMFSV 58

Qy 58 FDGHGGKLVAKFCAKHLHQEVVLKSEAYAKGDLKASLEYSF
 LRMDEMKGASGWKEL---
 Qy 59 YDGHGGEVALYCAYKLPDIKDKQAYKEGKLQKA
 LEFLDAFLAIDAKLTTEVIKELAQIA 118

Qy 114 - - - - -
 Db 119 GRPTEDEDEKEVADEDDVDNEEAALLHEATMTIEELTRYQ
 NCHKGPPHSKSGGGT 178

Qy 114 - - - - -
 Db 119 EEPGSQGLNGEAGPEDSTRETPSQENGPTAKAYTGFS
 SSNSERGTEAGQVGEPIPTGEAG 238

Qy 137 - - - - -
 Db 139 PSCSSASDQLPRAVAKSKFFEDSEDESDEAE
 EEEEDGYSSEEAEENEEDEDTT 298

Qy 168 - - - - -
 Db 299 EEAEEDEEEEMMVPGMEGKEPEGS
 DSDGTAVVALIRGNKLFVANAGDSRCIMSRGE 202

Qy 203 AVNLSIDHKPNLEHERKRRIESAGGFV-HGGRVNGSLNLT
 RAIGDMEFKGRPDLLPKQVV 261
 Db 359 ALDMSYDHKPEDEVELARIKNAGKVTMDGRVNGGLNLSRA
 IGDHFYKRNKNLPPPEQMI 418

Qy 262 TCCPDVVEDLGPGDEFIVIACDGIWDMSSQAVDFVKSRLP
 ---TTKTLSSLCEE 315

Db 419 SALPDIKVTLTDDHEFMVIA
 CDGINVMSSQEVVDFIQSISKISQRDENGLRLSSIVE 478

Qy 316 ILDYCLSP-TTRQEGCDNMSIIIV 339
 Db 479 LLDCQCLAPTSGDTGCDNMTCII 503

RESULT 2
 P2CG_MOUSE ID P2CG_MOUSE STANDARD; PRT; 542 AA.
 AC Q61074;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein phosphatase 2C gamma isoform (EC 3.1.3.16) (PP2C-gamma)
 DE (Protein phosphatase magnesium-dependent 1 gamma) (Protein phosphatase
 1C) (Fibroblast growth factor inducible protein 13) (FIN13).
 DE PM1G OR PM1C OR FIN13.
 OS Mus musculus (Mouse).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TAXID=10090;
 RN [1] SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.
 RP MEDLINE=97415625; PubMed=9271424;
 RA Guthridge M.A., Bellosta P., Tavoloni N., Basilico C.;
 RT "FIN13, a novel growth factor-inducible serine-threonine phosphatase
 which can inhibit cell cycle progression."
 RL Mol. Cell. Biol. 17:5485-5498(1997).
 RN [2] SEQUENCE OF 123-420 FROM N.A.
 RP MEDLINE=96226358; PubMed=864829;
 RX Guthridge M.A., Seldin M., Seldin M., Basilio C.;
 RA "Induction of expression of growth-related genes by FGF-4 in mouse
 fibroblasts."
 RT Oncogene 12:1267-1278(1996).
 RL -!- FUNCTION: MAY BE INVOLVED IN REGULATION OF CELL CYCLE.
 CC -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
 CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
 CC -!- COFACTOR: BINDS 2 MAGNESIUM IONS (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS. LOW LEVEL OF
 CC EXPRESSION IN KIDNEY. ALSO EXPRESSED IN A NUMBER OF TISSUES
 CC UNDERGOING PROLIFERATION INCLUDING EMBRYO, UTERUS AT PREGNANCY,
 CC PLACENTA, AND OVARIES.
 CC -!- INDUCTION: BY FIBROBLAST GROWTH FACTOR 4 AND SERUM.
 CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.

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CC DR EMBL; U42383; AAC26322.1; -.
 CC DR HSSP; P35813; 1A6Q.
 CC DR MGD; MGI:106065; Ppm1g.
 CC DR InterPro; IPR000222; PP2C.
 CC DR InterPro; IPR001932; PP2C_domain.
 CC DR Pfam; PF00481; PP2C; 2.
 CC DR SMART; SM00331; PP2C_SIG; 1.
 CC DR SMART; SM00332; PP2CC; 1.
 CC DR PROSITE; PS01032; PP2C; 1.
 CC KW Hydrolase; Magnesium; Manganese; Multigene family; Nuclear protein;
 CC KW Metal-binding; Cell cycle.
 CC FT METAL 40 40 MANGANESE 1 (BY SIMILARITY).
 CC FT METAL 41 41 MANGANESE 1 (BY SIMILARITY).
 CC FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
 CC FT METAL 438 438 MANGANESE 2 (BY SIMILARITY).
 CC FT METAL 493 493 MANGANESE 2 (BY SIMILARITY).
 CC FT DOMAIN 258 319 ASP/GLU-RICH (ACIDIC).
 CC FT CONFLICT 123 126 EDED -> NSAR (IN REF. 2).
 CC SQ SEQUENCE 542 AA; 58728 MW; 1DC72E7A66E71453 CRC64;

Query Match 34.9%; Score 641.5; DB 1; Length 542;
 Best Local Similarity 31.9%; Pred. No. 3.1e-42;
 Matches 161; Conservative 63; Mismatches 111; Indels 169; Gaps 9;

Qy 1 MGIYLCSPTKTDKTSEDDENA---ELRYGLSAMQGWRDMSMEDAHKA
 ILLNVDKNTSTSIFGI 57
 Db 1 MGAYLQSOPNTVKCGDGVGAPRLPLPYGFSAAMQGWRVSMEDAHNC
 IPFLD-SETAMFSV 58

Qy 58 FDGHGGKLVAKFCAKHLHQEVVLKSEAYAKGDLKASLEYSF
 LRMDEMKGASGWKEL---
 Qy 59 YDGHGGEVALYCAYKLPDIKDKQAYKEGKLQKA
 LEFLDAFLAIDAKLTTEVIKELAQIA 118

Qy 114 - - - - -
 Db 119 GRPTEDEDEKEVADEDDVDNEEAALLHEATMTIEELTRYQ
 NCHKGPPHSKSGGGT 178

Qy 114 - - - - -
 Db 119 EEPGSQGLNGEAGPEDSTRETPSQENGPTAKAYTGFS
 SSNSERGTEAGQVGEPIPTGEAG 238

Qy 137 - - - - -
 Db 139 PSCSSASDQLPRAVAKSKFFEDSEDESDEAE
 EEEEDGYSSEEAEENEEDEDTT 298

Qy 168 - - - - -
 Db 299 EEAEEDEEEEMMVPGMEGKEPEGS
 DSDGTAVVALIRGNKLFVANAGDSRCIMSRGE 202

Qy 203 AVNLSIDHKPNLEHERKRRIESAGGFV-HGGRVNGSLNLT
 RAIGDMEFKGRPDLLPKQVV 261
 Db 359 ALDMSYDHKPEDEVELARIKNAGKVTMDGRVNGGLNLSRA
 IGDHFYKRNKNLPPPEQMI 418

Qy 262 TCCPDVVEDLGPGDEFIVIACDGIWDMSSQAVDFVKSRLP
 ---TTKTLSSLCEE 315

Db 419 SALPDIKVTLTDDHEFMVIA
 CDGINVMSSQEVVDFIQSISKISQRDENGLRLSSIVE 478

Qy 316 ILDYCLSP-TTRQEGCDNMSIIIV 339
 Db 479 LLDCQCLAPTSGDTGCDNMTCII 503

RESULT 2
 P2CG_MOUSE ID P2CG_MOUSE STANDARD; PRT; 542 AA.
 AC Q61074;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein phosphatase 2C gamma isoform (EC 3.1.3.16) (PP2C-gamma)
 DE (Protein phosphatase magnesium-dependent 1 gamma) (Protein phosphatase
 1C) (Fibroblast growth factor inducible protein 13) (FIN13).
 DE PM1G OR PM1C OR FIN13.
 OS Mus musculus (Mouse).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TAXID=10090;
 RN [1] SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.
 RP MEDLINE=97415625; PubMed=9271424;
 RA Guthridge M.A., Bellosta P., Tavoloni N., Basilico C.;
 RT "FIN13, a novel growth factor-inducible serine-threonine phosphatase
 which can inhibit cell cycle progression."
 RL Mol. Cell. Biol. 17:5485-5498(1997).
 RN [2] SEQUENCE OF 123-420 FROM N.A.
 RP MEDLINE=96226358; PubMed=864829;
 RX Guthridge M.A., Seldin M., Seldin M., Basilio C.;
 RA "Induction of expression of growth-related genes by FGF-4 in mouse
 fibroblasts."
 RT Oncogene 12:1267-1278(1996).
 RL -!- FUNCTION: MAY BE INVOLVED IN REGULATION OF CELL CYCLE.
 CC -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
 CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
 CC -!- COFACTOR: BINDS 2 MAGNESIUM IONS (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS. LOW LEVEL OF
 CC EXPRESSION IN KIDNEY. ALSO EXPRESSED IN A NUMBER OF TISSUES
 CC UNDERGOING PROLIFERATION INCLUDING EMBRYO, UTERUS AT PREGNANCY,
 CC PLACENTA, AND OVARIES.
 CC -!- INDUCTION: BY FIBROBLAST GROWTH FACTOR 4 AND SERUM.
 CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.

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 entities requires a license agreement. (See http://www.isb-sib.ch/announce/
 or send an email to license@isb-sib.ch).

CC DR EMBL; U42383; AAC26322.1; -.
 CC DR HSSP; P35813; 1A6Q.
 CC DR MGD; MGI:106065; Ppm1g.
 CC DR InterPro; IPR000222; PP2C.
 CC DR InterPro; IPR001932; PP2C_domain.
 CC DR Pfam; PF00481; PP2C; 2.
 CC DR SMART; SM00331; PP2C_SIG; 1.
 CC DR SMART; SM00332; PP2CC; 1.
 CC DR PROSITE; PS01032; PP2C; 1.
 CC KW Hydrolase; Magnesium; Manganese; Multigene family; Nuclear protein;
 CC KW Metal-binding; Cell cycle.
 CC FT METAL 40 40 MANGANESE 1 (BY SIMILARITY).
 CC FT METAL 41 41 MANGANESE 1 (BY SIMILARITY).
 CC FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
 CC FT METAL 438 438 MANGANESE 2 (BY SIMILARITY).
 CC FT METAL 493 493 MANGANESE 2 (BY SIMILARITY).
 CC FT DOMAIN 258 319 ASP/GLU-RICH (ACIDIC).
 CC FT CONFLICT 123 126 EDED -> NSAR (IN REF. 2).
 CC SQ SEQUENCE 542 AA; 58728 MW; 1DC72E7A66E71453 CRC64;

Query Match 34.9%; Score 641.5; DB 1; Length 542;
 Best Local Similarity 31.9%; Pred. No. 3.1e-42;
 Matches 161; Conservative 63; Mismatches 111; Indels 169; Gaps 9;

Qy 1 MGIYLCSPTKTDKTSEDDENA---ELRYGLSAMQGWRDMSMEDAHKA
 ILLNVDKNTSTSIFGI 57
 Db 1 MGAYLQSOPNTVKCGDGVGAPRLPLPYGFSAAMQGWRVSMEDAHNC
 IPFLD-SETAMFSV 58

Qy 58 FDGHGGKLVAKFCAKHLHQEVVLKSEAYAKGDLKASLEYSF
 LRMDEMKGASGWKEL---
 Qy 59 YDGHGGEVALYCAYKLPDIKDKQAYKEGKLQKA
 LEFLDAFLAIDAKLTTEVIKELAQIA 118

Qy 114 - - - - -
 Db 119 GRPTEDEDEKEVADEDDVDNEEAALLHEATMTIEELTRYQ
 NCHKGPPHSKSGGGT 178

Qy 114 - - - - -
 Db 119 EEPGSQGLNGEAGPEDSTRETPSQENGPTAKAYTGFS
 SSNSERGTEAGQVGEPIPTGEAG 238

Qy 137 - - - - -
 Db 139 PSCSSASDQLPRAVAKSKFFEDSEDESDEAE
 EEEEDGYSSEEAEENEEDEDTT 298

Qy 168 - - - - -
 Db 299 EEAEEDEEEEMMVPGMEGKEPEGS
 DSDGTAVVALIRGNKLFVANAGDSRCIMSRGE 202

Qy 203 AVNLSIDHKPNLEHERKRRIESAGGFV-HGGRVNGSLNLT
 RAIGDMEFKGRPDLLPKQVV 261
 Db 359 ALDMSYDHKPEDEVELARIKNAGKVTMDGRVNGGLNLSRA
 IGDHFYKRNKNLPPPEQMI 418

Qy 262 TCCPDVVEDLGPGDEFIVIACDGIWDMSSQAVDFVKSRLP
 ---TTKTLSSLCEE 315

Db 419 SALPDIKVTLTDDHEFMVIA
 CDGINVMSSQEVVDFIQSISKISQRDENGLRLSSIVE 478

Qy 316 ILDYCLSP-TTRQEGCDNMSIIIV 339
 Db 479 LLDCQCLAPTSGDTGCDNMTCII 503

RESULT 2
 P2CG_MOUSE ID P2CG_MOUSE STANDARD; PRT; 542 AA.
 AC Q61074;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein phosphatase 2C gamma isoform (EC 3.1.3.16) (PP2C-gamma)
 DE (Protein phosphatase magnesium-dependent 1 gamma) (Protein phosphatase
 1C) (Fibroblast growth factor inducible protein 13) (FIN13).
 DE PM1G OR PM1C OR FIN13.
 OS Mus musculus (Mouse).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TAXID=10090;
 RN [1] SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.
 RP MEDLINE=97415625; PubMed=9271424;
 RA Guthridge M.A., Bellosta P., Tavoloni N., Basilico C.;
 RT "FIN13, a novel growth factor-inducible serine-threonine phosphatase
 which can inhibit cell cycle progression."
 RL Mol. Cell. Biol. 17:5485-5498(1997).
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 RP MEDLINE=96226358; PubMed=864829;
 RX Guthridge M.A., Seldin M., Seldin M., Basilio C.;
 RA "Induction of expression of growth-related genes by FGF-4 in mouse
 fibroblasts."
 RT Oncogene 12:1267-1278(1996).
 RL -!- FUNCTION: MAY BE INVOLVED IN REGULATION OF CELL CYCLE.
 CC -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
 CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
 CC -!- COFACTOR: BINDS 2 MAGNESIUM IONS (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS. LOW LEVEL OF
 CC EXPRESSION IN KIDNEY. ALSO EXPRESSED IN A NUMBER OF TISSUES
 CC UNDERGOING PROLIFERATION INCLUDING EMBRYO, UTERUS AT PREGNANCY,
 CC PLACENTA, AND OVARIES.
 CC -!- INDUCTION: BY FIBROBLAST GROWTH FACTOR 4 AND SERUM.
 CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.

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 entities requires a license agreement. (See http://www.isb-sib.ch/announce/
 or send an email to license@isb-sib.ch).

CC DR EMBL; U42383; AAC26322.1; -.
 CC DR HSSP; P35813; 1A6Q.
 CC DR MGD; MGI:106065; Ppm1g.
 CC DR InterPro; IPR000222; PP2C.
 CC DR InterPro; IPR001932; PP2C_domain.
 CC DR Pfam; PF00481; PP2C; 2.
 CC DR SMART; SM00331; PP2C_SIG; 1.
 CC DR SMART; SM00332; PP2CC; 1.
 CC DR PROSITE; PS01032; PP2C; 1.
 CC KW Hydrolase; Magnesium; Manganese; Multigene family; Nuclear protein;
 CC KW Metal-binding; Cell cycle.
 CC FT METAL 40 40 MANGANESE 1 (BY SIMILARITY).
 CC FT METAL 41 41 MANGANESE 1 (BY SIMILARITY).
 CC FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
 CC FT METAL 438 438 MANGANESE 2 (BY SIMILARITY).
 CC FT METAL 493 493 MANGANESE 2 (BY SIMILARITY).
 CC FT DOMAIN 258 319 ASP/GLU-RICH (ACIDIC).
 CC FT CONFLICT 123 126 EDED -> NSAR (IN REF. 2).
 CC SQ SEQUENCE 542 AA; 58728 MW; 1DC72E7A66E71453 CRC64;

Query Match 34.9%; Score 641.5; DB 1; Length 542;
 Best Local Similarity 31.9%; Pred. No. 3.1e-42;
 Matches 161; Conservative 63; Mismatches 111; Indels 169; Gaps 9;

Qy 1 MGIYLCSPTKTDKTSEDDENA---ELRYGLSAMQGWRDMSMEDAHKA
 ILLNVDKNTSTSIFGI 57
 Db 1 MGAYLQSOPNTVKCGDGVGAPRLPLPYGFSAAMQGWRVSMEDAHNC
 IPFLD-SETAMFSV 58

Qy 58 FDGHGGKLVAKFCAKHLHQEVVLKSEAYAKGDLKASLEYSF
 LRMDEMKGASGWKEL---
 Qy 59 YDGHGGEVALYCAYKLPDIKDKQAYKEGKLQKA
 LEFLDAFLAIDAKLTTEVIKELAQIA 118

Qy 114 - - - - -
 Db 119 GRPTEDEDEKEVADEDDVDNEEAALLHEATMTIEELTRYQ
 NCHKGPPHSKSGGGT 178

Qy 114 - - - - -
 Db 119 EEPGSQGLNGEAGPEDSTRETPSQENGPTAKAYTGFS
 SSNSERGTEAGQVGEPIPTGEAG 238

Qy 137 - - - - -
 Db 139 PSCSSASDQLPRAVAKSKFFEDSEDESDEAE
 EEEEDGYSSEEAEENEEDEDTT 298

Qy 168 - - - - -
 Db 299 EEAEEDEEEEMMVPGMEGKEPEGS
 DSDGTAVVALIRGNKLFVANAGDSRCIMSRGE 202

Qy 203 AVNLSIDHKPNLEHERKRRIESAGGFV-HGGRVNGSLNLT
 RAIGDMEFKGRPDLLPKQVV 261
 Db 359 ALDMSYDHKPEDEVELARIKNAGKVTMDGRVNGGLNLSRA
 IGDHFYKRNKNLPPPEQMI 418

Qy 262 TCCPDVVEDLGPGDEFIVIACDGIWDMSSQAVDFVKSRLP
 ---TTKTLSSLCEE 315

Db 419 SALPDIKVTLTDDHEFMVIA
 CDGINVMSSQEVVDFIQSISKISQRDENGLRLSSIVE 478

Qy 316 ILDYCLSP-TTRQEGCDNMSIIIV 339
 Db 479 LLDCQCLAPTSGDTGCDNMTCII 503

RESULT 2
 P2CG_MOUSE ID P2CG_MOUSE STANDARD; PRT; 542 AA.
 AC Q61074;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)

QY	144 SYAVLTERNSNLSNATKKHHKYSDFQGPIYYGSTAVVALIRGNKLFLVANAGDSRCIMSRGEA 203	Matches 164; Conservative 64; Mismatches 118; Indels 166; Gaps 10;
Db	299 EEA--EEDDEEMMVPGMEGKEEPGSDGTAVVALIRGNKLFLVANAGDSRCVVSEAGKA 356	QY 1 MGIVLCSPKTDKTSEDDENAE---RYGLSAMQGRWRSMEDAHKAILNVDKNTSTSIFGI 57
QY	204 VNLSIDHKPNEHERKRIESAGGGFV-HGGRVNGSLNLTRAIGDMEFKGRPDLPPDKQVVT 262	Db 1 MGAYLSQPNTVKCSGDGVASRLPYGFSAAMQGRWRSMEDAHNCIQELD--SETAMFSV 58
Db	357 LDMSYDHKPEDEVELARIKNAAGGKVTMMDGRVNGGLNLSRAIGDHFYKRKNKNLPPQEQMIS 416	QY 58 FDGHGGKLVAKFCAKHLLQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKELQLSL-
QY	263 CCPDVVEVDLGPGDEFIVLACDGIWDMVMSQAVVDFVKSRLP-----TTKTLSSLCEEI 316	QY 59 YDGHGGEELYCAKYLPPDIIKDQKAYKEGKLQKALEDAFLAIAKLTTEEVIKELAQIA 118
Db	417 ALPDIVKVLTLDDHEFMVIACDGIWNVMSQEVVDFIQSKISORDENGELRLLSSIVEEL 476	QY . 117 -----EETSQLDKL-----GNG 129
QY	317 LDYCLSP-TTROEQEGCDNMISIIIV 339	QY . 119 GRPTEDEKVADEDVDNEEAALLHEEATMTIEELLTRYQONCHKGAPHSKSGAGTG 178
Db	477 LDQCLAPDTSGDTGCDNMTCIII 500	QY 130 NS -----SSNAR----- 136
RESULT 3		
P2CG_BOVIN	STANDARD;	PRT; 543 AA.
ID P2CG_BOVIN		
AC P79126;		
DT 15-JUL-1998 (Rel. 36, Created)		QY 137 -----EDDESDSYAVLTVESNDNLATKKHVKYSDFQ----- 167
DT 15-JUL-1998 (Rel. 36, Last sequence update)		Db 239 PSCSSASDKLPRVDKSKFFEDSEDESDEAEEEEEESEEEDGYSSEAAENEEDDDT 298
DT 16-OCT-2001 (Rel. 40, Last annotation update)		QY 168 -----GPIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGEAV 204
DE Protein phosphatase 2C gamma isoform (EC 3.1.3.16) (PP2C-gamma)		Db 299 EAEEEDDEEEEMMVPGMEGKEEPGSDGTTAVVALIRGKQLIVANAGDSRCVVSEAGKAL 358
DE (Protein phosphatase magnesium-dependent 1 gamma) (Protein phosphatase DE 1B) (Magnesium-dependent calcium inhibitable phosphatase) (MCPP).		QY 205 NLSIDHKPNEHERKRIESAGGFV-HGGRVNGSLNLTRAIGDMEFKGRPDLPPDKQVVT 263
DE PPM1G OR PPM1C.		Db 359 DMSYDHKPEDDEVELARIKNAAGGKVTMMDGRVNGGLNLSRAIGDHFYKRKNKNLPPPEQMISA 418
GN OS taurus (Bovine).		QY 264 CPDVVEVDLGPGDEFIVLACDGIWDMVMSQAVVDFVKSRLP-----TTKTLSSLCEEIL 317
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;		Db 419 LPDIKVLTLDHEFWVIACDGIWNVMSQEVYDFIQSKISORDENGELRLLSSIVEYLL 478
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;		QY 318 DYCLSP-TTRQQEGCDNMISIIIVQPKQSGVAA 348
OC Bovidae; Bovinae; Bos.		Db 479 DQCLAPDTSGDTGCDNMTCIIIICFKPRNTAA 510
RN NCBI_TaxID=9913; [1]		
RP SEQUENCE FROM N.A.		
RA Huang C.Y.; Qin K.;		AC Q09172; P2C2_SCHPO STANDARD; PRT; 370 AA.
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.		DT 01-NOV-1995 (Rel. 32, Created)
CC -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +		DT 01-NOV-1995 (Rel. 32, Last sequence update)
CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).		DT 15-DEC-1998 (Rel. 37, Last annotation update)
CC -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).		DE Protein phosphatase 2C homolog 2 (EC 3.1.3.16) (PP2C-2).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).		GN PTC2 OR SPCC1223.11.
CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.		OS Schizosaccharomyces pombe (Fission yeast).
CC		OC Eukaryota; Fungi; Ascomycota; Schizosaccharomyces pombe;
CC		OC Schizosaccharomyctales; Schizosaccharomyctaceae;
CC		OC Schizosaccharomyces; Schizosaccharomyces pombe;
DR EMBL; U81159; AAB39357.1; -.		NCBI_TaxID=4896; OX
DR HSSP; P35813; 1A6Q; InterPro; IPR000222; PP2C.		RN [1] SEQUENCE FROM N.A.
DR InterPro; IPR001932; PP2C_domain.		RP STRAIN=972;
DR Pfam; PF00481; PP2C; 2.		RC MEDLINE=95163582; PubMed=7859738;
DR SMART; SM00331; PP2C_SIG; 1.		RA Shiozaki K.; Russell P.; RT "Counteractive roles of protein phosphatase 2C (PP2C) and a MAP kinase kinase homolog in the osmoregulation of fission yeast.".
DR PROSITE; PS01032; PP2C; 1.		RL EMBO J. 14:492-502(1995). [2] SEQUENCE FROM N.A.
KW Hydrolase; Magnesium; Manganese; Multigene family.		RP STRAIN=972; RA Wedler H., Wambutt R., Lyne M., Rajandream M.A., Barrell B.G., RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
FT METAL 40 40 Manganese 1 (BY SIMILARITY).		CC -!- FUNCTION: HAS AN IMPORTANT ROLE IN OSMOTIC STABILITY AND CELL SHAPE CONTROL. IT MAY NEGATIVELY REGULATE THE OSMOREGULATING SIGNAL
FT METAL 41 41 Manganese 1 (BY SIMILARITY).		CC TRANSMITTED THROUGH WIS1 MAP KINASE.
FT METAL 60 60 Manganese 1 AND 2 (BY SIMILARITY).		CC -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
FT METAL 439 439 Manganese 2 (BY SIMILARITY).		CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
FT METAL 494 494 Manganese 2 (BY SIMILARITY).		CC -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
FT DOMAIN 258 324 ASP/GLU-RICH ACIDIC.		CC -!- SUBUNIT: MONOMER.
FT DOMAIN 266 272 POLY-GLU.		
FT DOMAIN 306 309 POLY-GLU.		
SQ SEQUENCE 543 AA; 58708 MW; DD1898195E234A94 CRC64;		
Query Match Score 34.98; Best Local Similarity 32.08; Pred. No. 3.4e-42; Length 543;		

RA	Klumpp S., Hanke C., Donella-Deana A., Beyer A., Kellner R.,
RA	Pinna L.A., Schultz J.E.;
RT	"A membrane-bound protein phosphatase, type 2C from Paramecium tetraurelia. Purification, characterization, and cloning.";
J. Biol. Chem.	269:32774-32780(1994).
RL	-!- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
CC	-!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN + ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
CC	-!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC	-!- SUBCELLULAR LOCATION: Membrane-bound.
CC	-!- PTM: THE N-TERMINUS IS BLOCKED.
CC	-!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
DR	EMBL; Z36985; CAA85448.1; - .
DR	HSSP; P35813; 1A6Q.
DR	InterPro; IPR000222; PP2C.
DR	InterPro; IPR001932; PP2C_domain.
DR	Pfam; PF00481; PP2C; 1.
DR	SMART; SM00331; PP2C_SIG; 1.
DR	SMART; SM00332; PP2CC; 1.
DR	PROSITE; PS01032; PP2C; 1.
KW	Hydrolase; Magnesium; Manganese; Membrane.
FT	METAL 37 37 MANGANESE 1 (BY SIMILARITY).
FT	METAL 38 38 MANGANESE 1 (BY SIMILARITY).
FT	METAL 57 57 MANGANESE 1 AND 2 (BY SIMILARITY).
FT	METAL 237 237 MANGANESE 2 (BY SIMILARITY).
FT	METAL 289 289 MANGANESE 2 (BY SIMILARITY).
SQ	SEQUENCE 300 AA; 33739 MW; BC0318B4FF7724EC CRC64;
Query	Match 33.6%; Score 616.5; DB 1; Length 300;
Best Local Similarity 38.5%; Pred. No. 1.2e-40;	
Matches 132; Conservative 61; Mismatches 99; Indels 51; Gaps 4;	
Db	1 MGIYLCSPTDKTSEDDENAEELRYGLSAMQGWRDSMEDAHKAILNVDKNTSTSIFGIFDG 60 : : : : : : : : : : : 1 MGPYLSQPKRDKTTTGQGKSVIFAASEMQGWRNTMEDAH--IHRHDIIQDVSVFGVFDG 58
QY	61 HGGKLVAKEAKHLHQEVLKSEAYAKGDLKASLEYSSLRMDEMMKGASGMKELQSLEETS 120
Db	59 HGGREVAQFVEKHFVDELLFKNKNEKEQKFEEARLKEFLKMDELLTPEGQKELNQYKAT- 117
QY	121 SQLDKLGNGNSSSNAREDDDESVDYSAYVLTESNDSNLATKKHKYSDFQGPIYGSTAVVALI 180 : : : : : : : : : : : : Db 118 -----DTDESYA-----GCTANVALI 133
QY	181 RGNKLFVANAGDSRCIMSRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVNGSLNLT 240 : : : : : : : : : : : : Db 134 YKNTLYVANAGDSRSVLCRNNNTNHDMSSVDHKPDNPEEKSRIERAGGFVSDGRVNGNLNLS 193
QY	241 RAIGDMEFKGRPDLPDPDKQVVTCPPDVEVDLGPDEFIVLACDGIWDMSSQAVVDFVK 300 : : : : : : : : : : : : Db 194 RALGDLEYKRDNKLRSLRSNEQLLIALPDVKKTELTPQDKFILMGCDGVFETLNHQELLKQVN 253

01-NOV-1997 (Rel. 35, Last annotation update)
DE Protein phosphatase 2C homolog 3 (EC 3.1.3.16) (PP2C-3).
GN PTc3 OR SPAC2G11.07C.
OS Schizosaccharomyces pombe (Fission Yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosacharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1] SEQUENCE FROM N.A.
RP STRAIN=972;
RC RX MEDLINE=95163582; PubMed=7859738;
RA Shiozaki K.; Russell P.;
RT "Counteractive roles of protein phosphatase 2C (PP2C) and a MAP kinase homolog in the osmoregulation of fission yeast.";
RL EMBO J. 14:492-502(1995).
RN [2] SEQUENCE FROM N.A.
RC Badcock K.; Churcher C.M.; Barrell B.G.; Rajandream M.A.; Walsh S.V.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
CC !- FUNCTION: HAS AN IMPORTANT ROLE IN OSMOTIC STABILITY AND CELL SHAPE CONTROL. IT MAY NEGATIVELY REGULATE THE OSMORESENSING SIGNAL TRANSMITTED THROUGH WIS1 MAP KINASE.
CC -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN + ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
CC -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -!- SUBUNIT: MONOMER.
CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.

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DR EMBL; L34882; AAA67321.1;
DR EMBL; Z54354; CAA91172.1; -.
DR HSSP; P35813; 1A6Q.
DR InterPro; IPR00222; PP2C.
DR InterPro; IPR0019332; PP2C_domain.
DR Pfam; PE00481; PP2C; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR SMART; SM00332; PP2CC; 1.
DR PROSITE; PS01032; PP2C; 1.
DR KW hydrolase; Magnesium; Manganese; Multigene family.
FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
FT METAL 62 62 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 230 230 MANGANESE 2 (BY SIMILARITY).
FT METAL 279 279 MANGANESE 2 (BY SIMILARITY).
FT CONFLICT 196 196 K -> T (IN REF. 1).
SQ SEQUENCE 414 AA; 44856 MW; EFFF3A416625A2B11 CRC64;

Query Match 33.1%; Score 608.5; DB 1; Length 414;
Best Local Similarity 40.2%; Pred. No. 7.6e-40;
Matches 138; conservative 48; Mismatches 96; Indels 61; Gaps 5;

YQ 1 MGIVLCSPTKTDKTSEDDENAELRYGLSAMQWRDSMEDAHKAILNVDKNT---STSIFGI 57
DB 1 MGQTLSPEPVTEKHSVNGSNEFVLYGLSSMQRWISMEDAHSAILSMECSAVKDYPDFFAV 60

YQ 58 FDGHGGKLYAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGWKELOSLE 117
DB 61 YDGHGGDKVAKWCGSNLPQILEKNPDFQGDFVNALKSSFLNADKAI----- 107

YQ 118 ETSSQLDKLGNGNSSNAREDDESVDSYAVLTESNDNLATKKHHKYSDFQGPYIGSTAVV 177
DB 108 -----LDDQ-----FHTDPSGCTATV 124

Query Match 33.0%; Score 606; DB 1; Length 356;
Best Local Similarity 37.0%; Pred. No. 9.8e-40;
Matches 131; Conservative 58; Mismatches 103; Indels 62; Gaps 4;

YQ 1 MGIVLCSPTKTDKTSEDDENAELRYGLSAMQWRDSMEDAHKAILNVDKNTSTSIFGIFDG 60
DB 1 MGQTLSPEPVTEKHSVNGSNEFVLYGLSSMQRWISMEDAHSAILSMECSAVKDYPDFFAV 60

QY	61 HGGKLVAKFCAKHLHQEVVLKSEAYAKGDLKASLEYSFLRMDEMKGASGWKELOSLEETS	120	Matches 138; Conservative 65; Mismatches 132; Indels 149; Gaps 6;
Db	61 HGGSKVPSQYSGINLHKVVAQKEFSEGMRKAEIERKGFIELDQM-----	104	QY 1 MGIYLCSPKTDKTSEDDENAEILRYGLSAMQGWRDSMEDAHHKAIIINVDKNTSTSIFGGIFDG 60 Db 1 MGAYLNKPITEKEEGSGNGLSYACTTMQGWRVQNQDAHNCV--VDLHTDWFMGTVYDG 58
QY	121 SLDKLGNNSNAREDDESDSSYAVLTESNDSNLATKKHYSDEQQPIYGSTAVVALI	180	QY 61 HGGKLVAKFCAKHLHQEVVLKSEAYAKGDLKASLEYSFLRMDEMKGASGWKELOQ----- 114
Db	105 -----RVEDET-----	124	Db 59 HGGTEVSKFTSAKLPDFLKERKWEADDVAECLQKAFVDFDDFIRAEESMKELKDIGDEG 118
QY	181 RGNKLFVANAGDSRCIMSRRCGEAVNLSIDHKPNLEHERKRIESAGGFVHGGGRVNGSLNLT	240	QY 115 -----SLEETSSQLDK-----LGNGNSSSNARE 137
Db	125 KEGDVYCGNAGDSRAVSSVVGEARPLSFDHKPSHETEARRIIAAGGWVFEFNRVNGNLALS	184	Db 119 KPKKAGGEADSDEDADRITDIEASVPLAELLKRYGGAGVGKSLLSAFLAKGDVSDSSED 178
QY	241 RAIGDMEFKGRPDLPDKQVVTCPDPVVEVDLGPGEDEFIVLACDGIWDMSSQAVVDFVK	300	QY 138 DD-----
Db	185 RALGDFAFKNCDTKPAEEQIVTAFPDVITDKLTPDHEFTVLA CDGTWDMVMTNQEVVDFVR	244	Db 179 EDEDEEEAEEQDDTEEKKENEDASAEEVVIENADEKEEEQVDEEAEQDDEDAEDEQSDEEMVGDGL 238
QY	301 SRLPTTKTSSLCEELDYLCLSPTTRQEE-GCDNMSSIIVQPKQSGVAASSSTD	353	QY 140 -----ESD SYAVL TE ND SNL AT KK KY SD-----
Db	245 EKLAEKRDPOSICEELTRCLAPDCQMGGLQCDNNMTVVLV----GLLHGQSPD 293	165	Db 239 KSKSETDAETAPS SSSGVGVATEEEDDSDEEAEQDDEDAEDEQSDEEMVGDGL 298
RESULT 8	P2C1_CAEEL	STANDARD; PRT; 491 AA.	QY 166 -----FQGPIYGSTAVVALIRGKNLFVANAGDSRCIMSRRGEAVNLSIDHKPNL 214
ID	P2C1_CAEEL	STANDARD; PRT; 491 AA.	Db 299 APLLGSGGAEVPGEDSGTTACVCLYGDVKVIANAGDSRAVLCRNGKAVDLSYDHKPED 358
AC	P49595;		QY 215 EHERKRIESAGGFVHGGGRVNGSLNLT RAIGDMEFKGRPDLPDKQVVTCPDPVVEVDLGP 274
DT	01-FEB-1996 (Rel. 33, Created)		Db 359 EVETNRHAA GGQ1EDGRVNGLNL SRAFGDHA YKKNQELGLKEOMITALPDVKTEALTP 418
DT	01-OCT-1996 (Rel. 34, Last sequence update)		QY 275 GDEFIVLACDGIWDMSSQAVDFVKSRLPPTKTLSSLCEEILDYCLSPTT-RQQEGCDN 333
DT	01-NOV-1997 (Rel. 35, Last annotation update)		Db 419 EDEFIVVACDGINNSMESQQVVFVRIDLAKGSSCAEVCDALCDACLADSTDGDGTGCDN 478
DE	Probable protein phosphatase 2C F42G9.1 (EC 3.1.3.16) (PP2C).		QY 334 MSII 337
GN	F42G9.1.		Db 479 MTVI 482
OS	Caenorhabditis elegans.		RESULT 9
OC	Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;		P2C2_YEAST
OC	Rhabditidae; Peloderinae; Caenorhabditis.		ID P2C2_YEAST STANDARD; PRT; 464 AA.
NCBI_TAXID=6239; [1]	SEQUENCE FROM N.A. STRAIN-BRISTOL N2; Taich A., Waterston R.; Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.		AC P39966; DT 01-FEB-1995 (Rel. 31, Created)
RA	CC -1- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN + ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).		DT 01-FEB-1995 (Rel. 31, Last sequence update)
RA	CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).		DT 01-NOV-1997 (Rel. 35, Last annotation update)
RA	CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.		DE Protein phosphatase 2C homolog 2 (EC 3.1.3.16) (PP2C-2). GN PTC2 OR YER089C.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		OS Saccharomyces cerevisiae (Baker's yeast). OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces; Saccharomycetales; Saccharomycetaceae; Saccharomyces. OC NCBI_TaxID=4932; [1]
RN	RN SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RA Maeda T., Tsai A.Y.M., Saito H.; RL Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases. RN [2]		RP SEQUENCE FROM N.A. RA SEQUENCE FROM N.A. RL Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases. RN [2]
DR	DR STRAIN=S288C / AB972;		RP SEQUENCE FROM N.A. RC Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Aviles E., Berno A., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Guzman E., Hartzel G., Hunnicke-Smith S., Hyman R., Kayser A., Komp C., Lashkar D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.; RA Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases. RL -1- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN + ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC). CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY). CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
DR	DR SMART; SM00331; PP2C_SIG; 1.		CC this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
DR	DR SMART; SM00332; PP2CC; 1.		CC Best Local Similarity 30.3%; Score 55.5%; DB 1; Length 491;
DR	DR PROSITE; PS01032; PP2C; 1.		CC Pred. No. 1.2e-35;
DR	DR HYPOTHETICAL PROTEIN; HYDROLASE; MAGNESIUM; Manganese.		CC
KW	KW METAL 37 MANGANESE 1 (BY SIMILARITY).		CC
FT	FT METAL 38 MANGANESE 1 (BY SIMILARITY).		CC
FT	FT METAL 57 MANGANESE 1 AND 2 (BY SIMILARITY).		CC
FT	FT METAL 428 MANGANESE 2 (BY SIMILARITY).		CC
FT	FT METAL 477 MANGANESE 2 (BY SIMILARITY).		CC
SQ	SQ SEQUENCE 491 AA; 53141 MW; F110D12E343953D6 CRC64;		CC

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 CC or send an email to license@isb-sib.ch).
 CC

DR EMBL; U18839; AAB64644.1; - .
 DR HSSP; P35813; 1A6Q.
 DR SGD; S0000891; PTC2; .
 DR InterPro; IPR002222; PP2C.
 DR InterPro; IPR001932; PP2C_domain.
 DR Pfam; PF00481; PP2C; 1.
 DR SMART; SM00331; PP2C_SIG; 1.
 DR SMART; SM00332; PP2CC; 1.
 DR PROSITE; PS01032; PP2C; 1.
 KW Hydrolase; Magnesium; Manganese; Multigene family.
 FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
 FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
 FT METAL 62 62 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL ~ 234 234 MANGANESE 2 (BY SIMILARITY).
 FT METAL ~ 283 283 MANGANESE 2 (BY SIMILARITY).
 SQ SEQUENCE 464 AA; 50388 MW; 61D822CA4ED3FED CRC64;

Query Match 30.2%; Score 554.5; DB 1; Length 464;
 Best Local Similarity 36.8%; Pred. No. 1.3e-35; 7;
 Matches 133; Conservative 50; Mismatches 113; Indels 65; Caps 7;
 Query 1 MGIYLCPKTDKTSSEDDENAELRYGLSAMGWRDSMEDAHKAIIINV ---DKNTSTSIFG 56
 Db 1 MGQILSNPVIDKESHSAGDSLTAFLGLCAMGWRMSMEDSHILEPNVLTSDKD-HIAFYG 59
 Query 57 IFDGHGGKLVAKEFCAKHLQEVLKSEAYAKGDLKASLEYSFLRMDEMMKGASGMELQSL 116
 Db 60 IFDGHGGAKVAEYCGGNKIVEILQEKSFHEGNLPRALIDTFINTDVKLQLDPVMKE--- 115
 Query 117 EETSSQLDKLGNGNNSSNAREDESDESYAVLTESNDNLATKKHKYSDFQPIYGSTAV 176
 Db 116 -----DHS-----GCTAT 123
 Query 177 VALI--RGNKLFVNAGDSRCIMSRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVN 234
 Db 124 SILVSKSONLLVCGNAGDSRTVLATDGNAKALSYDHKPTLASEKSRIVAADGFVEMDRVN 183
 Query 235 GSLNLTRAIQDMEEFKGRPDLPDKQVVTCCPDVVEVDLG-PGDEFITVLACDGIWDMSSQ 293
 Db 184 GNLAISRAIGDFFEKSNPKLGPQEEQIVTCVPDILEHSLDYDRDEFVILACDGIWDCLTSG 243
 Query 294 AVVDFVKSRPLPTTKTSSLCEEILDYCLSPPTTRQQE-GCDNMSIIIVQPKQSGVAASSST 352
 Db 244 DCVDLVHGLREGKTLEIISRRIDVCCAPTEGTGIGCDNMSIIIVVALKEGEDVAQWS 303
 Query 353 D 353
 Db 304 D 304

RESULT 10
 ID P2CB_MOUSE STANDARD PRT; 390 AA.
 AC P36993;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein phosphatase 2C beta isoform (EC 3.1.3.16) (PP2C-beta) (IA)
 DE (Protein phosphatase 1B).
 GN PPM1B OR PPPM1B OR PP2C2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;

[1] RN SEQUENCE FROM N.A.
 RP MEDLINE=94099616; PubMed=8274020;
 RX RA Terasawa T., Kobayashi T., Murakami T., Ohnishi M., Kato S.,
 RA Tanaka O., Kondo H., Yamamoto H., Takeuchi T., Tamura S.;
 RT "Molecular cloning of a novel isotype of Mg(2+)-dependent protein
 RT phosphatase beta (type 2C beta) enriched in brain and heart.";
 RL Arch. Biochem. Biophys. 307:342-349(1993).
 RN [2] RN SEQUENCE FROM N.A. (BETA-3; BETA-4 AND BETA-5).
 RC TISSUE=Testis;
 RX MEDLINE=95251388; PubMed=7733667;
 RA Kato S., Terasawa T., Kobayashi T., Ohnishi M., Sasahara Y.,
 RA Kusuda K., Yanagawa Y., Hiraga A., Matsui Y., Tamura S.;
 RT "Molecular cloning and expression of mouse Mg(2+)-dependent protein
 RT phosphatase beta-4 (type 2C beta-4);"
 RL Arch. Biochem. Biophys. 318:387-393(1995).
 RN [3] RN SEQUENCE FROM N.A. (BETA-3 AND BETA-4).
 RP TISSUE=Testis;
 RC MEDLINE=94313028; PubMed=8038726;
 RA RA HOU E.W., Kawai Y., Miyasaka H., Li S.S.;
 RT "Molecular cloning and expression of cDNAs encoding two isoforms of
 RT protein phosphatase 2C beta from mouse testis.";
 RL Biochem. Mol. Biol. Int. 32:773-780(1994).
 RN [4] RN SEQUENCE FROM N.A.
 RP STRAIN=129/SV;
 RC MEDLINE=99398339; PubMed=10469137;
 RA Ohnishi M., Chida N., Kobayashi T., Wang H., Ikeda S., Hanada M.,
 RA Yanagawa Y., Katsura K., Hiraga A., Tamura S.;
 RT "Alternative promoters direct tissue-specific expression of the mouse
 RT protein phosphatase 2Cbeta gene.";
 RL Eur. J. Biochem. 263:736-745(1999).
 CC --!- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
 CC --!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
 CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
 CC --!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
 CC --!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC --!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; BETA-1 (SHOWN HERE), BETA-2,
 CC BETA-3, BETA-4 AND BETA-5; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC THEY ONLY DIFFER IN THEIR C-TERMINUS.
 CC --!- TISSUE SPECIFICITY: BETA-1 IS EXPRESSED UNIQUITUOUSLY; BETA-2 IS
 CC EXPRESSED EXCLUSIVELY IN BRAIN AND HEART; BETA-4 IS EXPRESSED
 CC EXCLUSIVELY IN BRAIN AND INTESTINE; BETA-3 AND BETA-5 ARE
 CC EXPRESSED EXCLUSIVELY IN TESTIS AND INTESTINE.
 CC --!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC

DR EMBL; D17411; BAA04233.1; - .
 DR EMBL; D17412; BAA04234.1; - .
 DR EMBL; D45859; BAA08293.1; - .
 DR EMBL; D45860; BAA08294.1; - .
 DR EMBL; D45861; BAA08295.1; - .
 DR EMBL; U09218; AAB60442.1; - .
 DR EMBL; AB007798; BAA84471.1; - .
 DR EMBL; AB007794; BAA84471.1; JOINED.
 DR EMBL; AB007795; BAA84471.1; JOINED.
 DR EMBL; AB007796; BAA84471.1; JOINED.
 DR EMBL; AB007797; BAA84471.1; JOINED.
 DR PIR; S39780; S39780.
 DR HSSP; P35813; 1A6Q.
 DR MGD; MGI:101841; Ppm1b.
 DR InterPro; IPR000222; PP2C.
 DR InterPro; IPR001932; PP2C_domain.
 DR Pfam; PF00481; PP2C; 1.

DR SMART; SM00331; PP2C_SIG; 1.
 DR SMART; SM00332; PP2C; 1.
 DR PROSITE; PS01032; PP2C; 1.
 KW Hydrolase; Magnesium; Manganese; Multigene family;
 Alternative splicing.
 FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
 FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
 FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 243 243 MANGANESE 2 (BY SIMILARITY).
 FT VARSPLIC 379 390 MANGANESE 2 (BY SIMILARITY).
 FT VARSPLIC 379 390 GAGDLEDLSVAL -> VSLHLPKVLF (IN ISOFORM
 BETA-2).
 FT VARSPLIC 379 390 GAGDLEDLSVAL -> FYQPSIAYSDNVELL (IN
 ISOFORM BETA-3).
 FT VARSPLIC 379 390 GAGDLEDLSVAL -> MADLSTSICKPS (IN ISOFORM
 BETA-4).
 FT VARSPLIC 388 390 VAL -> FYQPSIAYSDNVELL (IN ISOFORM BETA-
 5).
 FT SEQUENCE 390 AA; 42795 MW; 255C97B4276189FD CRC64;

Query Match 29.4%; Score 539; DB 1; Length 390;
 Best Local Similarity 33.5%; Pred. No. 1.7e-34;
 Matches 124; Conservative 58; Mismatches 112; Indels 76; Gaps 6;

Qy 1 MGIYLCSPKTDKTSEDDENAEELRYGLSAMOGWRDSMEDAHKAILNWKNTST-SIFGIFD 59	Db 1 MGAFLDKPKTEKHNAHGAGNGLRYGLSSMQGVWVEMEDAHTAVVGIPHGLDNWSFFFAVYD 60
Qy 60 GHGGKLVAKFCAKHLHQEVLKSEAYAKGD-----LKASLEYSFRLRDEMMKGA 107	Db 61 GHAGSRVANYCSTHLLERHTTNEFRAADKSGSALEPSVESVKTGIRTGFLKIDEYMRNF 120
Qy 108 SGWKELQSQLEETSSQLDKLGNGNNSSSNAREDDDESVDSYAVLTERNSNDSNLATKKHKYSDFQ 167	Db 121 S-----DLRNQMDRS-----130
Qy 168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRGRGEAVNLSIDHKPNLEHERKRIESAGGF 227	Db 131 ---GSTAVGMVSPTHMYFINGDSRAVLCRNGQVCFTQDHKPCTQDHKPQNVEKERIQNAGGS 186
Qy 228 VHGGGRVNGSLNLTRAIGDMEFKGRPDLPPDKDQVYTCCPDVVEDLPGDGEFTIVLACDGIW 287	Db 187 VMIQRVNGSLAVSRAKGDPDYKCVDKGKPTEQLVSPPEVYEIVRAEEDDEFVVLACDGIW 246
Qy 288 DVMSSQAVDFVKSRLLPTKTLSSLCEILLDYCLSPTTRQOECDNMSIIIV---QPKQ 343	Db 247 DVMSSNEELCEFVKSRLEVSDDLENVCNWVWDTC LHKGSR----DNMSVVLVCFNSNAPKV 301
Qy 344 SGVAASSSTD 353	Db 302 SEEAVKRDSE 311

RESULT 11
 P2CB_HUMAN STANDARD PRT; 479 AA.
 ID P2CB_HUMAN STANDARD PRT; 479 AA.
 AC 075688;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein phosphatase 2C beta isoform (EC 3.1.3.16) (PP2C-beta).
 GN PPM1B OR PP2CB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Liver;
 RX MEDLINE-98348020; PubMed=9684878;
 RA Marely A.E., Kline A., Crabtree G., Sullivan J.E., Beri R.K.;
 RT "The cloning expression and tissue distribution of human PP2Cbeta."
 RESULT 12

RL FEBS Lett. 431:121-124 (1998).
 CC -!- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
 CC -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
 CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
 CC -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- ALTERNATIVE PRODUCTS: A NUMBER OF ISOFORMS SUCH AS BETA-X (SHOWN
 HERE) ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY DIFFER IN
 THEIR C-TERMINUS.
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART AND SKELETAL MUSCLE.
 CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -!
 DR EMBL; AJ005801; CAA06704.1; -
 DR HSSP; P35813; 1A6Q.
 DR MIM; 603770; -
 DR InterPro; IPR000222; PP2C.
 DR InterPro; IPR001932; PP2C_domain.
 DR Pfam; PF00481; PP2C; 1.
 DR SMART; SM00331; PP2C_SIG; 1.
 DR SMART; SM00332; PP2C; 1.
 DR PROSITE; PS01032; PP2C; 1.
 KW Hydrolase; Magnesium; Manganese; Multigene family;
 KW Alternative splicing.
 FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
 FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
 FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT VARSPLIC 379 390 MANGANESE 2 (BY SIMILARITY).
 FT VARSPLIC 379 390 GAGDLEDLSVAL -> VSLHLPKVLF (IN ISOFORM
 BETA-2).
 FT VARSPLIC 379 390 GAGDLEDLSVAL -> FYQPSIAYSDNVELL (IN
 ISOFORM BETA-3).
 FT VARSPLIC 379 390 GAGDLEDLSVAL -> MADLSTSICKPS (IN ISOFORM
 BETA-4).
 FT VARSPLIC 388 390 VAL -> FYQPSIAYSDNVELL (IN ISOFORM BETA-
 5).
 FT SEQUENCE 390 AA; 42795 MW; 255C97B4276189FD CRC64;

Query Match 29.3%; Score 538; DB 1; Length 479;
 Best Local Similarity 34.6%; Pred. No. 2.6e-34;
 Matches 128; Conservative 57; Mismatches 109; Indels 76; Gaps 7;

Qy 1 MGIYLCSPKTDKTSEDDENAEELRYGLSAMOGWRDSMEDAHKAILNWKNTST-SIFGIFD 59	Db 1 MGAFLDKPKTEKHNAHGAGNGLRYGLSSMQGVWVEMEDAHTAVVGIPHGLDNWSFFFAVYD 60
Qy 60 GHGGKLVAKFCAKHLHQEVLKSEAYAKGD-----LKASLEYSFRLRDEMMKGA 107	Db 61 GHAGSRVANYCSTHLLERHTTNEFRAADKSGSALEPSVESVKTGIRTGFLKIDEYMRNF 120
Qy 108 SGWKELQSQLEETSSQLDKLGNGNNSSSNAREDDDESVDSYAVLTERNSNDSNLATKKHKYSDFQ 167	Db 121 S-----DLRNQMDRS-----130
Qy 168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRGRGEAVNLSIDHKPNLEHERKRIESAGGF 227	Db 131 ---GSTAVGMVSPTHMYFINGDSRAVLCRNGQVCFTQDHKPCTQDHKPQNVEKERIQNAGGS 186
Qy 228 VHGGGRVNGSLNLTRAIGDMEFKGRPDLPPDKDQVYTCCPDVVEDLPGDGEFTIVLACDGIW 287	Db 187 VMIQRVNGSLAVSRAKGDPDYKCVDKGKPTEQLVSPPEVYEIVRAEEDDEFVVLACDGIW 246
Qy 288 DVMSSQAVDFVKSRLLPTKTLSSLCEILLDYCLSPTTRQOECDNMSIIIV---QPKQ 343	Db 247 DVMSSNEELCEFVKSRLEVSDDLENVCNWVWDTC LHKGSR----DNMSVVLVCFNSNAPKV 301
Qy 344 SGVAASSSTD 353	Db 302 SEEAVKRDSE 311

Query Match 29.3%; Score 538; DB 1; Length 479;
 Best Local Similarity 34.6%; Pred. No. 2.6e-34;
 Matches 128; Conservative 57; Mismatches 109; Indels 76; Gaps 7;

Qy 1 MGIYLCSPKTDKTSEDDENAEELRYGLSAMOGWRDSMEDAHKAILNWKNTST-SIFGIFD 59	Db 1 MGAFLDKPKTEKHNAHGAGNGLRYGLSSMQGVWVEMEDAHTAVVGIPHGLDNWSFFFAVYD 60
Qy 60 GHGGKLVAKFCAKHLHQEVLKSEAYAKGD-----LKASLEYSFRLRDEMMKGA 107	Db 61 GHAGSRVANYCSTHLLERHTTNEFRAADKSGSALEPSVESVKTGIRTGFLKIDEYMRNF 120
Qy 108 SGWKELQSQLEETSSQLDKLGNGNNSSSNAREDDDESVDSYAVLTERNSNDSNLATKKHKYSDFQ 167	Db 121 S-----DLRNQMDRS-----130
Qy 168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRGRGEAVNLSIDHKPNLEHERKRIESAGGF 227	Db 131 ---GSTAVGMVSPTHMYFINGDSRAVLCRNGQVCFTQDHKPCTQDHKPQNVEKERIQNAGGS 186
Qy 228 VHGGGRVNGSLNLTRAIGDMEFKGRPDLPPDKDQVYTCCPDVVEDLPGDGEFTIVLACDGIW 287	Db 187 VMIQRVNGSLAVSRAKGDPDYKCVDKGKPTEQLVSPPEVYEIVRAEEDDEFVVLACDGIW 246
Qy 288 DVMSSQAVDFVKSRLLPTKTLSSLCEILLDYCLSPTTRQOECDNMSIIIV---QPKQ 343	Db 247 DVMSSNEELCEFVKSRLEVSDDLENVCNWVWDTC LHKGSR----DNMSVVLVCFNSNAPKV 301
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Qy 60 GHGGKLVAKFCAKHLHQEVLKSEAYAKGD-----LKASLEYSFRLRDEMMKGA 107	Db 61 GHAGSRVANYCSTHLLERHTTNEFRAADKSGSALEPSVESVKTGIRTGFLKIDEYMRNF 120
Qy 108 SGWKELQSQLEETSSQLDKLGNGNNSSSNAREDDDESVDSYAVLTERNSNDSNLATKKHKYSDFQ 167	Db 121 S-----DLRNQMDRS-----130
Qy 168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRGRGEAVNLSIDHKPNLEHERKRIESAGGF 227	Db 131 ---GSTAVGMVSPTHMYFINGDSRAVLCRNGQVCFTQDHKPCTQDHKPQNVEKERIQNAGGS 186
Qy 228 VHGGGRVNGSLNLTRAIGDMEFKGRPDLPPDKDQVYTCCPDVVEDLPGDGEFTIVLACDGIW 287	Db 187 VMIQRVNGSLAVSRAKGDPDYKCVDKGKPTEQLVSPPEVYEIVRAEEDDEFVVLACDGIW 246
Qy 288 DVMSSQAVDFVKSRLLPTKTLSSLCEILLDYCLSPTTRQOECDNMSIIIV---QPKQ 343	Db 247 DVMSSNEELCEFVKSRLEVSDDLENVCNWVWDTC LHKGSR----DNMSVVLVCFNSNAPKV 301
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 Matches 128; Conservative 57; Mismatches 109; Indels 76; Gaps 7;

Qy 1 MGIYLCSPKTDKTSEDDENAEELRYGLSAMOGWRDSMEDAHKAILNWKNTST-SIFGIFD 59	Db 1 MGAFLDKPKTEKHNAHGAGNGLRYGLSSMQGVWVEMEDAHTAVVGIPHGLDNWSFFFAVYD 60
Qy 60 GHGGKLVAKFCAKHLHQEVLKSEAYAKGD-----LKASLEYSFRLRDEMMKGA 107	Db 61 GHAGSRVANYCSTHLLERHTTNEFRAADKSGSALEPSVESVKTGIRTGFLKIDEYMRNF 120
Qy 108 SGWKELQSQLEETSSQLDKLGNGNNSSSNAREDDDESVDSYAVLTERNSNDSNLATKKHKYSDFQ 167	Db 121 S-----DLRNQMDRS-----130
Qy 168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRGRGEAVNLSIDHKPNLEHERKRIESAGGF 227	Db 131 ---GSTAVGMVSPTHMYFINGDSRAVLCRNGQVCFTQDHKPCTQDHKPQNVEKERIQNAGGS 186
Qy 228 VHGGGRVNGSLNLTRAIGDMEFKGRPDLPPDKDQVYTCCPDVVEDLPGDGEFTIVLACDGIW 287	Db 187 VMIQRVNGSLAVSRAKGDPDYKCVDKGKPTEQLVSPPEVYEIVRAEEDDEFVVLACDGIW 246
Qy 288 DVMSSQAVDFVKSRLLPTKTLSSLCEILLDYCLSPTTRQOECDNMSIIIV---QPKQ 343	Db 247 DVMSSNEELCEFVKSRLEVSDDLENVCNWVWDTC LHKGSR----DNMSVVLVCFNSNAPKV 301
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Qy 60 GHGGKLVAKFCAKHLHQEVLKSEAYAKGD-----LKASLEYSFRLRDEMMKGA 107	Db 61 GHAGSRVANYCSTHLLERHTTNEFRAADKSGSALEPSVESVKTGIRTGFLKIDEYMRNF 120
Qy 108 SGWKELQSQLEETSSQLDKLGNGNNSSSNAREDDDESVDSYAVLTERNSNDSNLATKKHKYSDFQ 167	Db 121 S-----DLRNQMDRS-----130
Qy 168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRGRGEAVNLSIDHKPNLEHERKRIESAGGF 227	Db 131 ---GSTAVGMVSPTHMYFINGDSRAVLCRNGQVCFTQDHKPCTQDHKPQNVEKERIQNAGGS 186
Qy 228 VHGGGRVNGSLNLTRAIGDMEFKGRPDLPPDKDQVYTCCPDVVEDLPGDGEFTIVLACDGIW 287	Db 187 VMIQRVNGSLAVSRAKGDPDYKCVDKGKPTEQLVSPPEVYEIVRAEEDDEFVVLACDGIW 246
Qy 288 DVMSSQAVDFVKSRLLPTKTLSSLCEILLDYCLSPTTRQOECDNMSIIIV---QPKQ 343	Db 247 DVMSSNEELCEFVKSRLEVSDDLENVCNWVWDTC LHKGSR----DNMSVVLVCFNSNAPKV 301
Qy 344 SGVAASSSTD 353	Db 302 SEEAVKRDSE 311

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 Matches 128; Conservative 57; Mismatches 109; Indels 76; Gaps 7;

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Qy 60 GHGGKLVAKFCAKHLHQEVLKSEAYAKGD-----LKASLEYSFRLRDEMMKGA 107	Db 61 GHAGSRVANYCSTHLLERHTTNEFRAADKSGSALEPSVESVKTGIRTGFLKIDEYMRNF 120
Qy 108 SGWKELQSQLEETSSQLDKLGNGNNSSSNAREDDDESVDSYAVLTERNSNDSNLATKKHKYSDFQ 167	Db 121 S-----DLRNQMDRS-----130
Qy 168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRGRGEAVNLSIDHKPNLEHERKRIESAGGF 227	Db 131 ---GSTAVGMVSPTHMYFINGDSRAVLCRNGQVCFTQDHKPCTQDHKPQNVEKERIQNAGGS 186
Qy 228 VHGGGRVNGSLNLTRAIGDMEFKGRPDLPPDKDQVYTCCPDVVEDLPGDGEFTIVLACDGIW 287	Db 187 VMIQRVNGSLAVSRAKGDPDYKCVDKGKPTEQLVSPPEVYEIVRAEEDDEFVVLACDGIW 246
Qy 288 DVMSSQAVDFVKSRLLPTKTLSSLCEILLDYCLSPTTRQOECDNMSIIIV---QPKQ 343	Db 247 DVMSSNEELCEFVKSRLEVSDDLENVCNWVWDTC LHKGSR----DNMSVVLVCFNSNAPKV 301
Qy 344 SGVAASSSTD 353	Db 302 SEEAVKRDSE 311

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 Best Local Similarity 34.6%; Pred. No. 2.6e-34;
 Matches 128; Conservative 57; Mismatches 109; Indels 76; Gaps 7;

Qy 1 MGIYLCSPKTDKTSEDDENAEELRYGLSAMOGWRDSMEDAHKAILNWKNTST-SIFGIFD 59	Db 1 MGAFLDKPKTEKHNAHGAGNGLRYGLSSMQGVWVEMEDAHTAVVGIPHGLDNWSFFFAVYD 60
Qy 60 GHGGKLVAKFCAKHLHQEVLKSEAYAKGD-----LKASLEYSFRLRDEMMKGA 107	Db 61 GHAGSRVANYCSTHLLERHTTNEFRAADKSGSALEPSVESVKTGIRTGFLKIDEYMRNF 120
Qy 108 SGWKELQSQLEETSSQLDKLGNGNNSSSNAREDDDESVDSYAVLTERNSNDSNLATKKHKYSDFQ 167	Db 121 S-----DLRNQMDRS-----130
Qy 168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRGRGEAVNLSIDHKPNLEHERKRIESAGGF 227	Db 131 ---GSTAVGMVSPTHMYFINGDSRAVLCRNGQVCFTQDHKPCTQDHKPQNVEKERIQNAGGS 186
Qy 228 VHGGGRVNGSLNLTRAIGDMEFKGRPDLPPDKDQVYTCCPDVVEDLPGDGEFTIVLACDGIW 287	Db 187 VMIQRVNGSLAVSRAKGDPDYKCVDKGKPTEQLVSPPEVYEIVRAEEDDEFVVLACDGIW 246
Qy 288 DVMSSQAVDFVKSRLLPTKTLSSLCEILLDYCLSPTTRQOECDNMSIIIV---QPKQ 343	Db 247 DVMSSNEELCEFVKSRLEVSDDLENVCNWVWDTC LHKGSR----DNMSVVLVCFNSNAPKV 301
Qy 344 SGVAASSSTD 353	Db 302 SEEAVKRDSE 311

Query Match 29.3%; Score 538; DB 1; Length 479;
 Best Local Similarity 34.6%; Pred. No. 2.6e-34;
 Matches 128; Conservative 57; Mismatches 109; Indels 76; Gaps 7;

Qy 1 MGIYLCSPKTDKTSEDDENAEELRYGLSAMOGWRDSMEDAHKAILNWKNTST-SIFGIFD 59	Db 1 MGAFLDKPKTEKHNAHGAGNGLRYGLSSMQGVWVEMEDAHTAVVGIPHGLDNWSFFFAVYD 60
Qy 60 GHGGKLVAKFCAKHLHQEVLKSEAYAKGD-----LKASLEYSFRLRDEMMKGA 107	Db 61 GHAGSRVANYCSTHLLERHTTNEFRAADKSGSALEPSVESVKTGIRTGFLKIDEYMRNF 120
Qy 108 SGWKELQSQLEETSSQLDKLGNGNNSSSNAREDDDESVDSYAVLTERNSNDSNLATKKHKYSDFQ 167	Db 121 S-----DLRNQMDRS-----130
Qy 168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRGRGEAVNLSIDHKPNLEHERKRIESAGGF 227	Db 13

P2CB_BOVIN STANDARD; PRT; 387 AA.
 ID P2CB_BOVIN ; STANDARD; PRT; 387 AA.
 AC 062830;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein phosphatase 2C beta isoform (EC 3.1.3.16) (PP2C-beta).
 GN PPMIB.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=98146173; PubMed=9486768;
 RA Klumpp S., Selke D., Fischer D., Baumann A., Mueller F., Thanos S.;
 RT "Protein phosphatase type-2C isozymes present in vertebrate retinae;
 purification, characterization, and localization in photoreceptors.",
 RL J. Neurosci. Res. 51:328-338(1998).
 CC -!- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
 CC -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
 CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
 CC -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AJ005458; CAA06555.1; -.
 DR HSSP; P35813; 1AQ0.
 DR InterPro; IPR00222; PP2C.
 DR InterPro; IPR001932; PP2C_domain.
 DR PFam; PF00481; PP2C; 1.
 DR SMART; SM00331; PP2C_SIG; 1.
 DR SMART; SM00332; PP2CC; 1.
 DR PROSITE; PS01032; PP2C; 1.
 KW Hydrolase; Magnesium; Manganese; Multigene family.
 FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
 FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
 FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 243 243 MANGANESE 2 (BY SIMILARITY).
 FT METAL 286 286 MANGANESE 2 (BY SIMILARITY).
 SQ SEQUENCE 387 AA; 42834 MW; D70B95141250FFB1 CRC64;

Query Match 29.2%; Score 537; DB 1; Length 387;
 Best Local Similarity 34.9%; Pred. No. 2.4e-34;
 Matches 129; Conservative 56; Mismatches 109; Indels 76; Gaps 7;

QY 1 MGIVLCSPKTDKTSSEDDENAEELRYGLSAMQGWRDSMEDAHKATLNVDKNTST-SIFGIFD 59
 Db 1 MGAFLDKPKTEKHAGAGNGLRYGLSSMQGWRVEMEDAHTAVVGIPHGLEDWSSFFAVYD 60

QY 60 GHGGKLVAKECAKHLHQEVLKSEAY-AKGDLKASLEY-----FLRMDDEMKGA 107
 Db 61 GHAGSRVANYCSTHLLEHITNNEDFRAAGKSGSALEPSVENVKNGIRTGFLKIDEYMRNF 120

QY 108 SGWKELQSLETSSQOLDKLGNNGNNSSSNAREDDESDSYAVLTESNDSNLATKKHYSDFQ 167
 Db 121 S-----DLRNQMDRS----- 130

Query Match 29.2%; Score 537; DB 1; Length 387;
 Best Local Similarity 34.9%; Pred. No. 2.4e-34;
 Matches 129; Conservative 56; Mismatches 109; Indels 76; Gaps 7;

QY 1 MGIVLCSPKTDKTSSEDDENAEELRYGLSAMQGWRDSMEDAHKATLNVDKNTST-SIFGIFD 59
 Db 1 MGAFLDKPKTEKHAGAGNGLRYGLSSMQGWRVEMEDAHTAVVGIPHGLEDWSSFFAVYD 60

QY 60 GHGGKLVAKECAKHLHQEVLKSEAY-AKGDLKASLEY-----FLRMDDEMKGA 107
 Db 61 GHAGSRVANYCSTHLLEHITNNEDFRAAGKSGSALEPSVENVKNGIRTGFLKIDEYMRNF 120

QY 108 SGWKELQSLETSSQOLDKLGNNGNNSSSNAREDDESDSYAVLTESNDSNLATKKHYSDFQ 167
 Db 121 S-----DLRNQMDRS----- 130

Query Match 29.2%; Score 537; DB 1; Length 387;
 Best Local Similarity 34.9%; Pred. No. 2.4e-34;
 Matches 129; Conservative 56; Mismatches 109; Indels 76; Gaps 7;

QY 168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRGEAVNLSDHKPNLEHERKRIESAGGF 227
 Db 131 ---GSTAVGVMSPKHIYFINGDSRAVLYRSQVCFSTQDHKPNCNPREKERIQNAGGS 186

QY 228 VHGGRVNGSLNLTRAIGDMEEFKGRPDLPPDKQVVTCCPDVVEVLGPGDEFITVLACDGIW 287
 Db 187 VMIQRYNGSLAVSRLPTKTLSSCEILDYCLSPTEQLVSPEPEVYEILRAEEDDEFITLACDGIW 246

QY 288 DVMSSQAVVDFVKSRLPTKTLSSCEILDYCLSPTEQLVSPEPEVYEILRAEEDDEFITLACDGIW 343
 Db 247 DVMNEELCEFVKSRLEVSDDLENVCNWVVDTCLHKGSR----DNMSIVLVCFSNAPKV 301

QY 344 SGVAASSSTD 353
 Db 302 SDEAMRKDSE 311

RESULT 13
 P2C3_YEAST
 ID P2C3_YEAST STANDARD; PRT; 468 AA.
 AC P34221; Q923330;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Protein Phosphatase 2C homolog 3 (EC 3.1.3.16) (PP2C-3).
 GN PTC3 OR YBL056W OR YBL0511 OR YBL0513.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 NCBI_TaxID=4932;

RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=S288C;
 RC RA Maeda T., Wurlger-Murphy S.M., Saito H.;
 RX RL Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
 RA RA Scherens B., el Bakkoury M., Vierendeels F., Dubois E., Messenguy F.;
 CC -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
 CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
 CC -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.

RN [2]
 RN SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RC RA Maeda T., Wurlger-Murphy S.M., Saito H.;
 RX RL Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
 RA RA Scherens B., el Bakkoury M., Vierendeels F., Dubois E., Messenguy F.;
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 CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.

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 RC RA Maeda T., Wurlger-Murphy S.M., Saito H.;
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 RA RA Scherens B., el Bakkoury M., Vierendeels F., Dubois E., Messenguy F.;
 CC -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
 CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
 CC -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.

RN [2]
 RN SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RC RA Maeda T., Wurlger-Murphy S.M., Saito H.;
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 CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
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 CC -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.

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 RP SEQUENCE FROM N.A.
 RC RA Maeda T., Wurlger-Murphy S.M., Saito H.;
 RX RL Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
 RA RA Scherens B., el Bakkoury M., Vierendeels F., Dubois E., Messenguy F.;
 CC -!- CATAL

Query Match	29.2%; Score 537; DB 1; Length 468;	Best Local Similarity 38.8%; Pred. No. 3e-34;	Mismatches 109; Indels 66; Gaps 9;
Db	1 MGOILSNPIIDKEHHSGTDCLTAFGLCAMOGWRMSMEDAHIVEPNLALAESDEEHLAFYGI 60		
Qy	1 MGIYLCSPTKTDKTSEDDENAELRYGLSAMQWRDSMEDAH---KAILNVDKNTSTSIFGI 57		
Db	1 MGOILSNPIIDKEHHSGTDCLTAFGLCAMOGWRMSMEDAHIVEPNLALAESDEEHLAFYGI 60		
Qy	58 FDGHGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSELFRMD-EMMKGASGWKELQLSL 116		
Db	61 FDGHGGSSVAEFGSKMISIILKKQESFKSGMLEQCLIDTFLATDVELLKD----- 110		
Qy	117 EETSSQQLDKLNGNNSNSNAREDDDESYYAVLTESNDNLATKKHYSDFQGPYIGSTAV 176		
Db	111 - -----EKL-----KDDHS-----GCTAT 123		
Qy	177 VALIRGNK~-LFVANAGDSRCIMSRGEAVNLSIDHKPNLEHERKRIESAGGGFVHGGRVN 234		
Db	124 VILVSQLKKLLICANSGDSRTVLSTGGNSKAMSFDHKPTLSEKSRIVAADGFVEMDRVN 183		
Qy	235 GSLNLTRAIQDMEEFKGRPDLPDKQWVTCPPDVVEVDLG-PGDEFIVLACDGIWWDVMSQQ 293		
Db	184 GNLAALSRAIGDFFEEKSNTNKLGPHEQVVTCVPDIICHNLNYDEFVILACDGIWWDCLTSQ 243		
Qy	294 AVVDEYKSRRLPT-TKTLSSLCCEEILDYCLSLSPPTTRQQE-GCDNMSIIIV 339		
Db	244 ECVDLVHYGISQGMNTLSDISSRIVDVCCSPTTEGSGIGCDNMSISIV 291		
RESULT 14			
P2CB_RAT	ID P2CB_RAT STANDARD; PRT; 390 AA.		
AC P35815; Q64046;	SEQUENCE FROM N.A. (ISOFORM BETA-1).		
DT 01-JUN-1994 (Rel. 29, Created)	TISSUE-Liver;		
DT 01-JUN-1994 (Rel. 29, Last sequence update)	MEDLINE-92201367; PubMed=1312947;		
DT 16-OCT-2001 (Rel. 40, Last annotation update)	Protein phosphatase 2C beta isoform (EC 3.1.3.16) (PP2C-beta) (IA)		
DE Protein phosphatase 2C beta isoform (EC 3.1.3.16) (PP2C-beta)	(Protein phosphatase 1B).		
DE PPM1B OR PPPM1B OR PP2C2.	Rattus norvegicus (Rat).		
GN Rattus norvegicus (Rat).	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;		
OS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	OC NCBI_TAXID=10116;		
OX	NCBI_TAXID=10116;		
RN [1]	SEQUENCE FROM N.A. (ISOFORM BETA-1).		
RP	"Monoclonal anti-FLAG antibodies react with a new isoform of rat Mg 2+ dependent protein phosphatase beta."		
RC	Biochem. Biophys. Res. Commun. 207:708-714(1995).		
RT	"Monoclonal anti-FLAG antibodies react with a new isoform of rat Mg 2+ dependent protein phosphatase beta."		
CC	- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.		
CC	- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN + ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).		
CC	- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).		
CC	- SUBUNIT: MONOMER (BY SIMILARITY).		
CC	- ALTERNATIVE PRODUCTS: A NUMBER OF ISOFORMS SUCH AS BETA-1 (SHOWN HERE) AND BETA-MPP ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY DIFFER IN THEIR C-TERMINUS.		
CC	- SIMILARITY: BELONGS TO THE PP2C FAMILY.		
RC	SEQUENCE FROM N.A.		
RX	Medline=95169115; PubMed=7532404;		
RA	Schafer K., Braun T.;		
RT	"Monoclonal anti-FLAG antibodies react with a new isoform of rat Mg 2+ dependent protein phosphatase beta."		
RL	Biochem. Biophys. Res. Commun. 207:708-714(1995).		
CC	- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.		
CC	- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN + ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).		
CC	- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).		
CC	- SUBUNIT: MONOMER (BY SIMILARITY).		
CC	- ALTERNATIVE PRODUCTS: A NUMBER OF ISOFORMS SUCH AS BETA-1 (SHOWN HERE) AND BETA-MPP ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY DIFFER IN THEIR C-TERMINUS.		
CC	- SIMILARITY: BELONGS TO THE PP2C FAMILY.		
RESULT 15			
P2CA_RAT	ID P2CA_RAT STANDARD; PRT; 382 AA.		
AC P20650;	01-FEB-1991 (Rel. 17, Created)		
DT 01-FEB-1991 (Rel. 17, Last sequence update)			
DT 15-JUL-1999 (Rel. 38, Last annotation update)			
DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha) (IA)			
DE (protein phosphatase 1A).			
GN PPM1A OR PPPM1A OR PP2C1.			
OS Rattus norvegicus (Rat).			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		

OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Db	301	AVKKEAE 307
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	[1]			
RN	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RP	TISSUE=Kidney;			
RX	Medline=89184515; PubMed=2538815;			
RA	Tamura S., Lynch K.R., Larner J., Fox J., Yasui A., Kikuchi K., Suzuki Y., Tsuiki S.;			
RA	"Molecular cloning of rat type 2C (IA) protein phosphatase mRNA."			
RT	Proc. Natl. Acad. Sci. U.S.A. 86:1796-1800(1989).			
RL	-!- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.			
CC	-!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN + ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).			
CC	-!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS.			
CC	-!- SUBUNIT: MONOMER.			
CC	-!- SIMILARITY: BELONGS TO THE PP2C FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; J04503; AAA41917.1; -.			
CC	DR; P32399; A32399.			
CC	DR; P35813; 1A6Q.			
DR	InterPro; IPR000222; PP2C.			
DR	InterPro; IPR001932; PP2C_domain.			
DR	PFam; PF00481; PP2C; 1.			
DR	SMART; SM00331; PP2C_SIG; 1.			
DR	SMART; SM00332; PP2CC; 1.			
DR	PROSITE; PS01032; PP2C; 1.			
KW	Hydrolase; Magnesium; Manganese; Multigene family.			
FT	METAL 37 37 MANGANESE 1 (BY SIMILARITY).			
FT	METAL 38 38 MANGANESE 1 (BY SIMILARITY).			
FT	METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).			
FT	METAL 239 239 MANGANESE 2 (BY SIMILARITY).			
FT	METAL 282 282 MANGANESE 2 (BY SIMILARITY).			
SQ	SEQUENCE 382 AA; 42416 MW; C1C386E935374F89 CRC64;			
Query Match	28.4%; Score 522; DB 1; Length 382;			
Best Local Similarity	34.1%; Pred. No. 3.3e-33;			
Matches 125; Conservative	59; Mismatches 109; Indels 74; Gaps 9;			
Qy	1 MGIYLCSPKTDKTSEDDENAEELRYGLSAMQWRDSDMEDAHKAIIINVDKNTST-SIEGFIFD 59			
Db	1 MGAFLDKPKMEKHNAAQGQNGNLRYGLSSMQWRVEMEDAHTAVIGLPSGLETWSEFFAVYD 60			
Qy	60 GHGGKLVAKPCAKHLHQEVLKSEAYAKG-----DLKASLEYSLFLRMDDEMMKGASGWK 111			
Db	61 GHAGSQWAKYCCEHLLDHITNNQDF-KGSAGAPSVENVKNGIRTGFLEIDEHMR----- 113			
Qy	112 ELQSLETSSQQLKGNGNSSSNAREDDDESVDYSAYVLTESNDSNLATKKHKSDFQGPYI 171			
Db	114 -----VMSE-----KKH-----GADRS 125			
Qy	172 GSTAVVALIRGNKLFVANAGDSRCIMSRGEAVNLIDHKPNLEHERKRIESAGGFVHGG 231			
Db	126 GSTAVGVLLISPOQHTYFINCGDSRGLLCRNRKVHFFTQDHKPSNPLEKERIONAGGSVMIQ 185			
Qy	232 RVNGSLNLTRAIGDMEFKGRPDLPFDKQVWTCCPDPVVEVDLG-PGDEFIVLACDGIWDM 290			
Db	186 RVNGSLPAVSRALGDFDYKCVHGRGPTEQLVSPEPEVHDITERSEEDDQFILACDGIWDM 245			
Qy	291 SSQAVVDFVKSRLPTTKTLSSILCEIILDCCLSPTTRQQEGCDNMIIIV---QPKQSGV 346			
Db	246 GNEELCDFYRSRLEVTDDELCYKVCNEVVDTCLYKGSR----DNMSVILICFPNAPKVSAE 300			
Qy	347 AASSSTD 353			

H84643 probable protein phosphatase 2C [imported] - *Arabidopsis thaliana*
 C; Species: *Arabidopsis thaliana* (mouse-ear cress)
 C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 15-Jun-2001
 C; Accession: H84643
 R; Lin, X.; Kaul, S.; Rounslley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-769, 1999
 A; Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A; Reference number: A84420; MUID:20083487
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-355 <STO>
 A; Cross-references: GB:AE002093; NID:g4559345; PIDN:AAD23006.1; GSPDB:GN00139
 C; Genetics:
 A; Gene: At2g25070
 A; Map position: 2
 C; Superfamily: human phosphoprotein phosphatase 1A

Query Match 52.7%; Score 967; DB 2; Length 355;
 Best Local Similarity 53.3%; Pred. No. 3.5e-70; Gaps 2;
 Matches 188; Conservative 60; Mismatches 93; Indels 12; Gaps 2;

Qy 1 MGIVLCSPIKTDKTSEDDENAEELRYGLSAMQGRDMSMEDAHKAILNSTDHKPNEHERKRRIESAGGFVHGGRVN 234
 Db 1 MGTYLSSPKTEKLSEDGENDKLRFLGQLSSMQWRATMDEHAAILDLD--DKTSEFFGVYDG 58

Qy 61 HGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMKGASGWKELOSLEETS 120
 Db 59 HGGKVVAKFCAKYLHQQVISNEAKRTGDVEITSRLRAAFFRMDMMQGQRGWRELAVLGDKM 118

Qy 121 SQLDKLGNGNNSSNAREDDESDYSYAVLTESNDNLATKKHYSDFQGPPIYGSTA 175
 Db 106 -----NALMQDR-----DMQEDPSGCTA 123

Qy 176 VVALIRGNK-LFVANAGDSRCIMSRGEAVNLSTDHKPNEHERKRRIESAGGFVHGGRVN 234
 Db 124 TTALIVDHQVIVYCANAGDSRTVLGRKGTAEPLSFDHKPNNDEKARITAAGGF1DFGRVN 183

Qy 235 GSLNLTRAIGDMEFKGRPDLPDPDKQVYTCCPDPVVEVDLGPQDEFIVLACDGITWDYMSQQA 294
 Db 184 GSLALSRAGDFEYKKDSSLPEKQIVTAFDPLVHNIDPDEFILACDGITWDCKSSQQ 243

Qy 295 VVDFVKSRSLPPTKTLSSLCEETILDYCLSPPTTRQ-QEGCDNMSSIIV 339
 Db 244 VVEFVRGIVARQSLLEVICENLMRDCAIASNSESCGIGCDNMWTICIV 289

RESULT 4

A55804 181 RGNKLFVANAGDSRCIMSRGEAVNLSTDHKPNEHERKRRIESAGGFVHGGRVNGSLNL 240
 Db 169 KDKKLFVANAGDSRCIVSRKSQAYNLSKDHPDLEVERILRKAGGF1HAGRINGSLNLT 228

Qy 241 RAIGDMEFKGRPDLPDKQVVTCPDPDVVEVDLGPQDEFIVLACDGITWDVMSQAVVDFVK 300
 Db 229 RAIGDMEFKQNKFELPSEKQMVTAQDPDINTIDLCDDDFLVACDGIWDCMSQELVDFIH 288

Qy 301 SRLPTTKTLSSLCEETILDYCLSPPTTRQEGCDNMSSIIVQPKQSGVVAASSSTD 353
 Db 289 EQLKSETKLSTVCEKVKDRCLAPDTATGECCDNMTIILVQFKKPNPSETEPED 341

RESULT 3

S54297 protein phosphatase 2C homolog - fission yeast (*Schizosaccharomyces pombe*)
 C; Species: *Schizosaccharomyces pombe*
 C; Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 15-Jun-2001
 C; Accession: S54297; T40871
 R; Shiozaki, K.; Russell, P.
 A; Title: Counteractive roles of protein phosphatase 2C (PP2C) and a MAP kinase kinase kinase
 A; Reference number: S54297; MUID:95163582
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-370 <STO>
 A; Cross-references: EMBL:L34881; NID:g609655; PIDN:AAA67320.1; PID:g609656
 R; Wedler, H.; Wambutt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, September 1998
 A; Reference number: Z21953
 A; Accession: T40871
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-370 <WED>

Query Match 34.6%; Score 635; DB 2; Length 370;
 Best Local Similarity 41.6%; Pred. No. 2.1e-43; Mismatches 48; Indels 64; Gaps 8;
 Matches 144; Conservative 90; Gaps 8;

Qy 1 MGIVLCSPIKTDKTSEDDENAEELRYGLSAMQGRDMSMEDAHKAILN-VDKNTS---TSIFG 56
 Db 1 MGQTLSPEPVLDKHSSSGDRLHFGVSHMOGRWISMEDAHCALLNFTDSNNNNPPTSFVG 60

Qy 57 IFDGHGGKLVAKFCAKHLHQEVLKSE-AYAKGDLKASLEYFLRMDEMKGASGWKELOS 115
 Db 61 VFDGHGGDRYAKYCROHL-PDIKSQPSFWKGNYDEALKSGFLAAD----- 105

Qy 116 LEETSSQLDKLGNGNNSSNAREDDESDYSYAVLTESNDNLATKKHYSDFQGPPIYGSTA 175
 Db 106 -----NALMQDR-----DMQEDPSGCTA 123

Qy 176 VVALIRGNK-LFVANAGDSRCIMSRGEAVNLSTDHKPNEHERKRRIESAGGFVHGGRVN 234
 Db 124 TTALIVDHQVIVYCANAGDSRTVLGRKGTAEPLSFDHKPNNDEKARITAAGGF1DFGRVN 183

Qy 235 GSLNLTRAIGDMEFKGRPDLPDPDKQVYTCCPDPVVEVDLGPQDEFIVLACDGITWDYMSQQA 294
 Db 184 GSLALSRAGDFEYKKDSSLPEKQIVTAFDPLVHNIDPDEFILACDGITWDCKSSQQ 243

Qy 295 VVDFVKSRSLPPTKTLSSLCEETILDYCLSPPTTRQ-QEGCDNMSSIIV 339
 Db 244 VVEFVRGIVARQSLLEVICENLMRDCAIASNSESCGIGCDNMWTICIV 289

RESULT 4

A; Cross-references: GB:Z36985; NID:9537421; PID:e1192609; PID:92654382
 C; Genetics:
 A; Genetic code: SG5
 C; Keywords: phosphoric monoester hydrolase
 A; Molecule type: mRNA
 A; Residues: 1-300 <KLJU>
 A; Cross-references: GB:Z36985; NID:9537421; PID:e1192609; PID:92654382
 C; Genetics:
 A; Genetic code: SG5
 C; Keywords: phosphoric monoester hydrolase
 A; Molecule type: mRNA
 A; Residues: 1-300 <KLJU>

Query Match 33.6%; Score 616.5; DB 2; Length 300;
 Best Local Similarity 38.5%; Pred. No. 4.7e-42; Mismatches 61; Indels 51; Gaps 4;
 Matches 132; Conservative 99; Gaps 4;

Qy 1 MGIVLCSPIKTDKTSEDDENAEELRYGLSAMQGRDMSMEDAHKAILNVDKNTSTSIFGIFDG 60
 Db 1 MGPyLSSQPKRDKTTTQGQKSVFAASEMOGWRNTMEDAH-TIHRHDIIQDVSVFGVFDG 58

Qy 61 HGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYFLRMDEMKGASGWKELOSLEETS 120
 Db 59 HGGREVAQFVEKHFVDELLKNKNEKEQKFEEARKEFLKMDDELLTPEGQKELNQYKAT- 117

Qy 121 SQLDKLGNGNNSSNAREDDESDYSYAVLTESNDNLATKKHYSDFQGPPIYGSTA 180
 Db 118 -----DTDESYA-----GCTANVALI 133

QY	181	RGNKLFVANAGDSRCIMSRGEAVNLSIDHKPNLEHERKRIESAGGFVHGGRVNGSLNLIT	240	RESULT 6
Db	134	YKNTLYVANAGDSRSVLCRNNTNHDMSVDHKPDNEEKSRIERAGGFVSDGRYNGNLNLSS	193	E88434 protein T23F11.1 [imported] - Caenorhabditis elegans
QY	241	RAIGDMEFKGRPDLPDKQWVTCPPDVVEWLGPQDEFIVLACDGIWDMSSQAVVDFVK	300	C;Species: Caenorhabditis elegans
Db	194	RALGDLLEYKRDNKLRSLNEQLLIALPDVKKTELTPQDRFLMGCDGVETLNHQELLKQVN	253	C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 15-Jun-2001
QY	301	SRL----PTTKTTLSSLCEELDYLCLSPTTRQEQGCDNMSSIIV	339	C;Accession: E88434 R;anonymous, The C. elegans Sequencing Consortium.
Db	254	STIGQAQVTEELLKKAEDLLDQLLAPDTSQGTGCDNMNTTILV	296	R;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
				A;Reference number: A75000; MUID:99069613; PMID:9851916
				A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
				A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
				A;Accession: E88434
				A;Status: preliminary
				A;Molecule type: DNA
				A;Residues: 1-348 <STO>
				A;Cross-references: GB:chr_III; PIDN:CAA86456.1; PID:g3880103; GSPDB:GN00021; CESP:T23F11.1
				C;Genetics:
				A;Gene: T23F11.1
				A;Map Position: 3
				C;Superfamily: human phosphoprotein phosphatase 1A
				A;Accession: Z21745
				A;Status: preliminary; fission yeast (Schizosaccharomyces pombe)
				C;Species: Schizosaccharomyces pombe
				C;Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 15-Jun-2001
				C;Accession: T38573; S54298; S62462
				R;Baddock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
				submitted to the EMBL Data Library, October 1995
				A;Reference number: Z21745
				A;Accession: T38573
				A;Status: preliminary; translated from GB/EMBL/DDBJ
				A;Molecule type: DNA
				A;Residues: 1-414 <BA2>
				A;Cross-references: EMBL:254354; NID:91019398; PIDN:CAA91172.1; PID:g1019405; GSPDB:GN00021
				R;Shiozaki, K.; Russell, P.
				EMBO J. 14, 492-502, 1995
				A;Title: Counteractive roles of protein phosphatase 2C (PP2C) and a MAP kinase kinase kinase number: S54297; MUID:95163582
				A;Reference number: S54298
				A;Accession: S54298
				A;Status: preliminary
				A;Molecule type: DNA
				A;Cross-references: EMBL:L34882; NID:9609657; PIDN:AAA67321.1; PID:g609658
				C;Genetics:
				A;Gene: SPAC2G11.07C
				A;Map Position: 1L
				A;Introns: 110/1; 134/3
				C;Superfamily: human phosphoprotein phosphatase 1A
				A;Accession: T23F11.1
				A;Status: preliminary
				A;Molecule type: DNA
				A;Residues: 1-348 <STO>
				A;Cross-references: GB:chr_III; PIDN:CAA86456.1; PID:g3880103; GSPDB:GN00021; CESP:T23F11.1
				C;Genetics:
				A;Gene: CESP:T23F11.1
				A;Map Position: 3
				A;Introns: 35/1; 132/1; 207/1; 255/3; 280/3; 308/3; 332/1
				C;Superfamily: human phosphoprotein phosphatase 1A

Query Match	33.0%	Score 606; DB 2; Length 356;	Db	239 KSKSETDAETAPSSSSGVGVATEEEEDDSDEFVADEEEDEDAEDEQSDEEMVDSL 298
Best Local Similarity	37.0%	Pred. No. 4.2e-41;	Qy	166 -----FQGPIYGSTAVVALIRGNKLFVANAGDSRCIMSRGEAVNLSIDHKPNL 214
Matches 131; Conservative 58; Mismatches 103; Indels 62; Gaps 4;			Db	299 APLLGSAGAEPGEGSDTTACVCLVRNGKAVDLSVDHKPED 358
Qy 1 MGIYLCSPKTDKTSEDDENAELRYGLSAMOGWRDSMEDAHKA1LNVDKNTSTS1FG1FDG 60			Qy	215 EHERKRIESAGGFVHGRVNGSLNTRAIQDMEFKGRPDLPPDKQVVTCPDYVEVDLGP 274
Db 1 MGOTLSEPVTKKESASCANENLYVGSSCMQGWVMDMEDIATHLLSILPDPKCAFFAVYDG 60			Db	359 EVETNRIHAAGGQIEDGRVNGGLNLNSRAFGDHAYKKNQELGLKEQMITALPDVKIEALT P 418
Qy 61 HGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFRLDEMKGASGWKELQSLEETS 120			Qy	275 GDEFITVLACDGTWDVMSMSQAVVDFVKSRLPLPTKTLSSLCEELDYCLSPTT-RQQEGCDN 333
Db 61 HGGSKVSQYSGINLHKVVAQKEFSEGNMKBAIEKGFIELDQOM-----104			Db	419 EDEFIVVACDGTWMSQVQVDFVRDLAKGSSCAEVCDALCDACLAQSTDGDGTGCDN 478
Qy 121 SLDKLGNNSSSNAREDDES DY SYAVLTESNDSNLATKKHKSDFQGPIYGSTAVVALI 180			Qy	334 MSII 337
Db 105 -----RVDEET-----KDDVSGTAVVVL 124			Db	479 MTVI 482
Qy 181 RGNKLFVANAGDSRCIMSRGEAVNLSIDHKPNLEHERKRIESAGGFVHGRVNGSLNLT 240		RESULT 9	S50592	
Db 125 KEGDVYCGNAGDSRAVSSVVGEARPLSFHDHKPSHETEARRIIAAGGWWEFNRVNGNLALS 184				hypothetical protein YER089C - Yeast (Saccharomyces cerevisiae)
Qy 241 RAIGDMEFKGRPDLPPDKQVVTCPDPVVEVDLPGDEFIVLACDGIWDMSSQAVVDFVK 300			C; Species: Saccharomyces cerevisiae	
Db 185 RALGDFAFKNCDTKPAEEQIVTAFPDPVITDQLTPDHEFIVLACDGTWDMTNQEVVDFVR 244			C; Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 15-Jun-2001	
Qy 301 SRLPTTKTLSSLCLEEILDYCLSPTTRQE-GCDNMSTIIIVQPQSGYAAASSSTD 353			C; Accession: S50592	
Db 245 EKLAERKDPOQSIICEULLTRCLAPDCQMGGLCDNMNTVVVLV----GLLHGQSPD 293			R; Dietrich, F.S.	
Qy T16354			Submitted to the EMBL Data Library, December 1994	
C; Species: Caenorhabditis elegans			A; Description: The sequence of <i>S. cerevisiae</i> cosmids 9747, 8198, 9781, and lambda c10	
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999			A; Reference number: S50436	
C; Accession: T16354			A; Accession: S50592	
R; Taich, A.			A; Molecule type: DNA	
submitted to the EMBL Data Library, March 1996			A; Residues: 1-464 <DIE>	
A; Description: The sequence of <i>C. elegans</i> cosmid F42G9.			A; Cross-references: EMBL:U18839; NID:g6033313; PID:AAB64644.1; MIPS:YERO	
A; Reference number: Z18498			C; Genetics:	
A; Accession: T16354			A; Gene: SGD:PTC2	
A; Status: preliminary; translated from GB/EMBL/DDBJ			A; Cross-references: SGD:PTC2	
A; Molecule type: DNA			A; Map position: 5R	
A; Residues: 1-491 <TAI>			C; Superfamily: human phosphoprotein phosphatase 1A	
A; Experimental source: strain Bristol N2				
C; Genetics:				
A; Gene: CESP:F42G9.1				
A; Introns: 37/3; 254/2; 364/2; 406/2				
Qy T16354			Query Match 30.2%; Score 554.5; DB 2; Length 464;	
C; Species: Caenorhabditis elegans			Best Local Similarity 36.8%; Pred. No. 8.6e-37;	
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999			Mismatches 50; Indels 65; Gaps 7;	
C; Accession: T16354				
R; Taich, A.				
submitted to the EMBL Data Library, March 1996				
A; Description: The sequence of <i>C. elegans</i> cosmid F42G9.				
A; Reference number: Z18498				
A; Accession: T16354				
A; Status: preliminary; translated from GB/EMBL/DDBJ				
A; Molecule type: DNA				
A; Residues: 1-491 <TAI>				
A; Experimental source: strain Bristol N2				
C; Genetics:				
A; Gene: CESP:F42G9.1				
A; Introns: 37/3; 254/2; 364/2; 406/2				
Qy 1 MGIYLCSPKTDKTSEDDENAELRYGLSAMOGWRDSMEDAHKA1LNVDKNTSTS1FG1FDG 60			Qy 117 VALI--RGNKLFVANAGDSRCIMSRGEAVNLSIDHKPNLEHERKRIESAGGFVHGRVN 234	
Db 1 MGAYLNKP1IEKEKEEGSGNGLSYACTM0GWRVNOEDAHCNC~-VDLHTDWMFGVYDG 58			Db 116 -----DHS-----GCTAT 115	
Qy 61 HGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSFRLDEMKGASGWKELQ-----114			Qy 177 VALI--RGNKLFVANAGDSRCIMSRGEAVNLSIDHKPNLEHERKRIESAGGFVHGRVN 234	
Db 59 HGGTEVSKFTSAKLPDFLKERKFWEADDVAECLQKAFVDDFIRAEESMKELKDIGDEG 118			Db 124 SILVSKSQNLVCGNAGDSRTVLATDGNAKALSYDHKP1LASERK1VADGFVEMDRVN 183	
Qy 115 -----SLEETSSQLDK-----LGNGNNSSSNARE 137			Qy 235 GSLNLTRAIGDMEFKGRPDLPPDKQVVTCCPDPVVEVDLGL-PGDEFIVLACDGIWDMSSQ 293	
Db 119 KPKKAGGEADSEADRIDTIEASVPLAELLKRYGGAGVGSLLSAFLAKGDSDDSED 178			Db 184 GNLALSRAIGDGFEEFKSNPKLGPPEEQ1YTCVPDILEHSLDYDREFVILACDGIWDCLTSQ 243	
Qy 138 DD-----139			Qy 294 AVVDFVKSRLPPTKTLSSLCEEILDYCLSPTTRQQE-GCDNMSIIIVQPQKQSGVAASSST 352	
Db 179 EDEDEEEAEEQDDTEEKKENEDASAEEVVIENAEDKEEEEGLSPKKKGQKRCOKSPIQSEAK 238			Db 244 DCVDLVHLGLREKGTLNEISSRIIDVCCAPTEGGTGIGCDNMSIVVALLREGEDVAQWS 303	
Qy 140 -----ESDY SYAVLTESNDSNLATKKHKS D-----165			Qy 353 D 353	
Db 304 D 304			Db 304 D 304	

RESULT 10

S65672 phosphoprotein phosphatase (EC 3.1.3.16) 1A-beta-4 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 15-Jun-2001

C;Accession: S65672

R;Kato, S.; Terasawa, T.; Kobayashi, T.; Ohnishi, M.; Sasahara, Y.; Kusuda, K.; Yanagawa Arch. Biochem. Biophys. 318, 387-393, 1995

A;Title: Molecular cloning and expression of mouse Mg(2+)-dependent protein phosphatase A;Reference number: S65670; MUID:95251388

A;Accession: S65672

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-390 <KAT>

A;Cross-references: EMBL:D45860; NID:g961471; PIDN:BAA08294.1; PID:945252

C;Superfamily: human phosphoprotein phosphatase 1A

C;Keywords: phosphoric monoester hydrolase; serine/threonine-specific phosphatase

Query Match 29.4%; Score 539; DB 2; Length 390;

Best Local Similarity 33.5%; Pred. No. 1.2e-35;

Matches 124; Conservative 58; MisMatches 112; Indels 76; Gaps 6;

QY 1 MGIVLCSPKTDKTSEDDENAEILRYGLSAMQGWRDSMEDAHKAIIINVDKNTST-SIFGIFD 59

Db 1 MGAFLDKPKTEKHNAAHAGANGLRYGLSSMQGWRVEMEDAHTAVVGGIPHGLDNWSFEAVYD 60

QY 60 GHGGKLVAKECAKHLHQEVLKSEAYAKGD-----LKASLEYSFLRMDEMMKGA 107

Db 61 GHAGSRVANYCSTHLLIEHTTNEDERAADKSGSALEPSVESVKTGIRTGFLKRIDEYMRNF 120

QY 108 SGWKELOSLEETSSQOLDKGNGNNSSNAREDDESDYSYAVLTESNDNLATKKHKSDFQ 167

Db 121 S-----DLRNGMDRS----- 130

QY 168 GPIYGSTAVVALIRGNKLFVANAGDSRCIIMSRRGEAWNLISDHKPNEHERKRRIESAGGF 227

Db 131 -----GSTAVGVMVSPTHMYFINCGDSRAVLCRNGQVCFSTQDHKPCTNPVEKERIQNAGGS 186

QY 228 VHGGRVNGSLNLTRAIQDMFKGRPDLPDKQVVTCPPDVYEDLGPGDEFIVLACDGIW 287

Db 187 VMIQRVNGSLAVSRALGDYKCVDGKGPTEQLVSPPEVYEIVRAEEDFVVLACDGIW 246

QY 288 DVMSSQAVVDFVKSRLPTTKTLSSLCEELLDYCLSPTRQQEGCDNMSIIIV----QPKQ 343

Db 247 DVMSENELCEFVKSRLLEVSDDLENVCNWVVDTCLHKGSR-----DNMSVVLVCFSNAPKV 301

QY 344 SGVAASSSTD 353

Db 302 SEEAVKRDSE 311

RESULT 11

I49016 phosphoprotein phosphatase (EC 3.1.3.16) 1A - mouse

C;Species: Mus musculus (house mouse)

C;Accession: I49016; S65671; S39780; S39781

R;Hou, E.W.; Kawai, Y.; Miyasaka, H.; Li, S.S.

Arch. Biochem. Mol. Biol. Int. 32, 773-780, 1994

A;Title: Molecular cloning and expression of cDNAs encoding two isoforms of protein phosphatase number: I49016; MUID:94313028

A;Accession: I49016

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-393 <RES>

A;Cross-references: EMBL:U09218; NID:g484099; PIDN:AAB60442.1; PID:9484100

A;Experimental source: tissue testis

R;Kato, S.; Terasawa, T.; Kobayashi, T.; Ohnishi, M.; Sasahara, Y.; Kusuda, K.; Yanagawa Arch. Biochem. Biophys. 318, 387-393, 1995

A;Title: Molecular cloning and expression of mouse Mg(2+)-dependent protein phosphatase A;Reference number: S65670; MUID:95251388

A;Accession: S65671

A;Molecule type: mRNA

A;Residues: 1-378, 'GAGDLEDSSYAL' <TER>

A;Cross-references: GB:D17411; NID:9452525; PIDN:BAA04233.1; PID:945252

A;Accession: S39781

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-378, 'VSLHLPKYLK' <TER>

A;Cross-references: GB:D17412; NID:9452527; PIDN:BAA04234.1; PID:945252

C;Genetics:

A;Gene: PP2C

C;Superfamily: human phosphoprotein phosphatase 1A

C;Keywords: magnesium; phosphoric monoester hydrolase; serine/threonine-specific phosphatase; binding site: magnesium 1 (Glu, Asp, Asp) #status predicted F;60,243,286/Binding site: magnesium 2 (Asp) #status predicted

Query Match 29.4%; Score 539; DB 2; Length 393;

Best Local Similarity 33.5%; Pred. No. 1.2e-35;

Matches 124; Conservative 58; MisMatches 112; Indels 76; Gaps 6;

QY 1 MGIVLCSPKTDKTSEDDENAEILRYGLSAMQGWRDSMEDAHKAIIINVDKNTST-SIFGIFD 59

Db 1 MGAFLDKPKTEKHNAAHAGANGLRYGLSSMQGWRVEMEDAHTAVVGGIPHGLDNWSFEAVYD 60

QY 60 GHGGKLVAKECAKHLHQEVLKSEAYAKGD-----LKASLEYSFLRMDEMMKGA 107

Db 61 GHAGSRVANYCSTHLLIEHTTNEDERAADKSGSALEPSVESVKTGIRTGFLKRIDEYMRNF 120

QY 108 SGWKELOSLEETSSQOLDKGNGNNSSNAREDDESDYSYAVLTESNDNLATKKHKSDFQ 167

Db 121 S-----DLRNGMDRS----- 130

QY 168 GPIYGSTAVVALIRGNKLFVANAGDSRCIIMSRRGEAWNLISDHKPNEHERKRRIESAGGF 227

Db 131 -----GSTAVGVMVSPTHMYFINCGDSRAVLCRNGQVCFSTQDHKPCTNPVEKERIQNAGGS 186

QY 228 VHGGRVNGSLNLTRAIQDMFKGRPDLPDKQVVTCPPDVYEDLGPGDEFIVLACDGIW 287

Db 187 VMIQRVNGSLAVSRALGDYKCVDGKGPTEQLVSPPEVYEIVRAEEDFVVLACDGIW 246

QY 288 DVMSSQAVVDFVKSRLPTTKTLSSLCEELLDYCLSPTRQQEGCDNMSIIIV----QPKQ 343

Db 247 DVMSENELCEFVKSRLLEVSDDLENVCNWVVDTCLHKGSR-----DNMSVVLVCFNSAPKV 301

QY 344 SGVAASSSTD 353

Db 302 SEEAVKRDSE 311

RESULT 12

S39832 probable phosphoprotein phosphatase (EC 3.1.3.16) - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein YBL0513; hypothesis

C;Species: Saccharomyces cerevisiae

C;Date: 16-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 15-Jun-2001

C;Accession: S39832; S45791; S37333

R;Scherens, B.; el Bakkouri, M.; Vierendeels, F.; Dubois, E.; Messenguy, F.

Yeast 9, 1355-1371, 1993

A;Title: Sequencing and functional analysis of a 32 560 bp segment on the left arm of

A;Reference number: S39824; MUID:94205266

A;Accession: S39832

A;Molecule type: DNA

A; Residues: 1-468 <SCH>
A; Cross-references: EMBL:Z23261; NID:g313733; PIDN:CAA80791.1; PID:g313742
A; Experimental source: strain S288C
R; Dubois, E.; El Bakkoury, M.; Glansdorff, N.; Messenguy, F.; Pierard, A.; Scherens, B.; submitted to the Protein Sequence Database, August 1994
A; Reference number: S45782
A; Accession: S45791
A; Molecule type: DNA
A; Residues: 1-468 <DUB>
A; Cross-references: EMBL:Z35817; NID:g536085; PID:g536086; MIPS:YBL056w
A; Experimental source: strain S288C
C; Genetics:
A; Gene: SGD:PTC3
A; Cross-references: SGD:S0000152; MIPS:YBL056w
A; Map position: 2L
C; Superfamily: human phosphoprotein phosphatase 1A
C; Keywords: phosphoric monoester hydrolase; serine/threonine-specific phosphatase

Query Match 29.2%; Score 537; DB 2; Length 468;
Best Local Similarity 38.8%; Pred. No. 2.2e-35;
Matches 135; Conservative 38; Mismatches 109; Indels 66; Gaps 9;

Qy 1 MGIYLCSPTDKTSEDDENAEELRYGLSAMQGWRDSMEDAH--KAILNVDKNTSTSISFGI 57
Db 1 MGQILSNPIIDKEHHSGTDCLTAFGLCAMQGWRMSMEDAHTVEPNLALAESDEEHLAGFYGI 60

Qy 58 FDGHGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSLFLRMD-EMMKGASGWKELQSL 116
Db 61 FDGHGGSSVVAEFCGSKMISILKKQESFKSGMLEQCLIDTFLATDVELLKD-----
Db 111 - -----EKL-----KDDHS-----
Db 117 EETSSQLDKLGNGNSSSNAREDDESDYAVLTESNDSNLATKKHYSDFQGPIYGSTAV 176
Db 124 VILVSQLKKLLICANSGDSRTVLSGGNSKAMSFHDHKPTLSEKSRTIVAADGFVEMDRVN 183
Db 125 GSLNLTRAIGDMFKGGRPDLPDKQVVTCCPDPVVEVDLG-PGDEFIVLACDGIVWDVMSQ 293
Db 184 GNLAWSRAIGDFFEKSNKNTKLGPHEQVVTCPDIICHNLNYDEDEFVILACDGIVWLTSQ 243
Qy 235 GSLNLTRAIGDMFKGGRPDLPDKQVVTCCPDPVVEVDLG-PGDEFIVLACDGIVWDVMSQ 293
Db 124 AVVDFVKSRRLPT-TKTLSSLCEELDYCLSPTRQQE-GCDNMSIIIV 339
Db 244 ECVDLVHYGISQGNMTLSDISSRIVDVCCSPTEGSGIGCDNMSISIV 291

RESULT 13
S20392 Query Match 29.1%; Score 534; DB 2; Length 397;
A; Residues: 1-390 <WEN>
A; Cross-references: GB:S90449; NID:9247926; PIDN:AAB21898.1; PID:g247927
A; Molecule type: mRNA
A; Status: not compared with conceptual translation
A; Accession: S20392; MUID:92201367
A; Reference number: S20392
A; Superfamily: human phosphoprotein phosphatase 1A
C; Keywords: phosphoric monoester hydrolase; serine/threonine-specific phosphatase

Qy 1 MGIYLCSPTDKTSEDDENAEELRYGLSAMQGWRDSMEDAHKAILNVDKNTST-SIFGIFT 59
Db 1 MGAFLDKPKTEKHNAGANGLRYGLSSMQGWRVEMEDAHTAVVGIPHGLEDWSFFAVYD 60
Db 60 GHGGKLVAKFCAKHLHQEVLKSEAYAKGD-----LKAESLEYSLFLRMDDEMKGKA 107
Db 61 GHAGSRVANYCSTHLEHTTNEDERAADKSGFALEPSVENVKTGIRTGFLKIDEYMRNF 120
Db 108 SGWKELQSLEETSSQDKLGNGNSSSNAREDDESDYAVLTESNDSNLATKKHYSDFQ 167
Db 121 S-----DLRNGMDRS-----
Db 131 ----GSTAVGVNMISPTHIYFINCGDSRAVLCRNGQVCFSTQDHKPCNPMEKERIQNAGGS 186
Qy 1 MGIYLCSPTDKTSEDDENAEELRYGLSAMQGWRDSMEDAHKAILNVDKNTST-SIFGIFT 59
Db 128 VHGGRVNGSLNLTGMEFKGRPDLPDKQVVTCCPDPVVEVDLGPGDEFIVLACDGIV 287
Db 187 VMIQRVNGSLAVSRALGDDYKCVDGGKGPTEQLVSPEPEVYIELRAEEDFVVVLACDGIV 246

Query Match 29.1%; Score 534; DB 2; Length 390;
Best Local Similarity 34.3%; Pred. No. 3e-35;
Matches 125; Conservative 54; Mismatches 109; Indels 76; Gaps 6;

Qy 1 MGIYLCSPTDKTSEDDENAEELRYGLSAMQGWRDSMEDAHKAILNVDKNTST-SIFGIFT 59

search completed: June 19, 2002, 08:46:28
Job time: 222 sec

Gencore version 4.5
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OM protein - protein search, using sw model

Run on: June 19, 2002, 08:41:40 ; Search time 13.29 seconds
 (without alignments)
 648.776 Million cell updates/sec

Title: US-09-828-302-14

Perfect score: 1836
 Sequence: 1 MGIYLCSPTDKTSEDDENA.....MSIIIVQPQSGVAAASSSTD 353

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:
 1: /cggn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cggn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cggn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cggn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cggn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cggn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	64.3	35.0	546	3	US-08-935-855-20	Sequence 20, Appl
2	641.5	34.9	542	3	US-08-935-855-22	Sequence 22, Appl
3	538	29.3	478	2	US-08-873-093-1	Sequence 1, Appl
4	538	29.3	478	2	US-08-873-093-4	Sequence 4, Appl
5	534	29.1	390	2	US-08-873-093-3	Sequence 3, Appl
6	533.5	29.1	309	2	US-08-822-701-7	Sequence 7, Appl
7	533.5	29.1	309	3	US-08-935-855-7	Sequence 7, Appl
8	520	28.3	306	2	US-08-822-701-8	Sequence 8, Appl
9	520	28.3	306	3	US-08-935-855-8	Sequence 8, Appl
10	491.5	26.8	392	2	US-08-822-701-2	Sequence 2, Appl
11	491.5	26.8	392	3	US-08-935-855-2	Sequence 2, Appl
12	370.5	20.2	392	4	US-09-013-881-2	Sequence 2, Appl
13	341.5	18.6	281	2	US-08-822-701-9	Sequence 9, Appl
14	341.5	18.6	281	3	US-08-935-855-9	Sequence 9, Appl
15	326	17.8	314	2	US-08-822-701-10	Sequence 10, Appl
16	326	17.8	314	3	US-08-935-855-10	Sequence 10, Appl
17	156.5	8.5	504	2	US-08-752-891-2	Sequence 2, Appl
18	156.5	8.5	504	2	US-08-752-891-6	Sequence 6, Appl
19	156.5	8.5	504	2	US-09-144-178-2	Sequence 2, Appl
20	156.5	8.5	504	4	US-09-144-178-6	Sequence 6, Appl
21	156.5	8.5	504	4	US-09-406-854-2	Sequence 2, Appl
22	156.5	8.5	504	4	US-09-406-854-6	Sequence 6, Appl
23	97.5	5.3	15281	2	US-08-471-119A-2	Sequence 2, Appl
24	90	4.9	707	2	US-08-949-941B-2	Sequence 2, Appl
25	89	4.8	802	2	US-08-007-107-4	Sequence 4, Appl
26	88.5	4.8	1477	1	US-08-038-682-4	Sequence 4, Appl
27	88.5	4.8	1477	1	US-08-302-832-4	Sequence 4, Appl

Query Match Best Local Similarity 35.0%; Score 643; DB 3; Length 546;
 Matches 165; Conservative 60; Mismatches 112; Indels 168; Gaps 9;

SEQUENCE CHARACTERISTICS:
 LENGTH: 542 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Mus musculus
 US-08-935-855-22

Query Match 34.9%; Score 641.5; DB 3; Length 542;
 Best Local Similarity 31.9%; Pred. No. 1.3e-60;
 Matches 161; Conservative 63; Mismatches 111; Indels 169; Gaps 9;

QY 1 MGIYLCSPPKTDKTSEDDENA---ELRYGLSAMOGWRDSSMEDAHKAIIINVDKNTSTSIFGI 57
 Db 1 MGAYLSPQPTVKCGDGVAPLLPYGSAMQGWRVSMEDAHCPELD--SETAMFSV 58

QY 58 FDGHGGKLYAKFCAKHLHQEVLKASLEYAKGDLKASLEYSFRLMDEMMKGASGWKEL---- 113
 Db 59 YDGHGGEEVALYCAKYLPIIKDQKAYKEGKLQKALEDAFLAIDAKLTTEEVIKELAQIA 118
 Qy 114 ~----- 113

Db 119 GRPTEDDEKEVADEDDVDNEEAALLHEATMTIEELLTRYGQNCHKGPPHSKSGGGTG 178
 Qy 114 ~-----QSLEETSSQOLD---KLGNGNSSSNAR---- 136
 Db 179 EEPGSQQLNGEAGPDSRTPEQNGPTAKAYTGFESSNTERGEAG 238
 Qy 137 ~-----EDDESDSYAVLTERNSNDNLATKKHKSDFQ---- 167
 Db 239 PSCSSASDKLPRVAKSKFFEDSEDESDEAEEEEEEDEEDYSSSEEAAEENEEDEDTT 298
 Qy 168 ~-----GPIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGE 202
 Db 299 EAEEEDDEEEEMMVPGMEGKEPGSQDSGTAVVALIRGQLIVANAGDSRCVVSEAGK 358
 Qy 203 AVNLSIDHKPNLEHERKRIESAGGFV-HGGRVNGSLNLTRAIGDMEFKGRPDLPDKQVV 261
 Db 359 ALDMSYDHKPDEVELARIKNAGGKVTMGRVNGLNLNSRAIGDHFYKRKNKNLPPEEQMI 418
 Qy 262 TCCPDVVEVDLGPQDFEIVLACDGIWDMSSQAVVDFVKSRLP----TTKTLSSLCE 315
 Db 419 SALPDIKVLTLDHFEMVIACDGIWNVNMSSQEVVDFIQSKISKISQRDENGEPLLSSIVE 478
 Qy 316 ILDYCLSP-TTRQEQCDNMSIIIV 339
 Db 479 LLDQCLAPPDTSGDGTGCDNMTCIII 503

RESULT 2
 US-08-935-855-22
 ; Sequence 22, Application US/08935855
 ; Patent No. 6066485
 ; GENERAL INFORMATION:
 ; APPLICANT: Guthridge, Mark
 ; APPLICANT: Basilico, Claudio
 ; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
 ; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David A. Jackson, Esq.
 ; STREET: 411 Hackensack Ave, Continental Plaza, 4th
 ; STREET: Floor
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/935,855
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-487-5800
 ; TELEXFAX: 201-343-1684
 ; INFORMATION FOR SEQ ID NO: 22:
 ; RESULT 3
 ; US-08-873-093-1
 ; Sequence 1, Application US/08873093
 ; Patent No. 5853997
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Goli, Surya K.
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Zhang, Hong
 ; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/873,093
 FILING DATE: Filed Herewith
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0319 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: ~478 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: THPIPLB01
 CLONE: 13177
 US-08-873-093-1

Query Match 29.3%; Score 538; DB 2; Length 478;
 Best Local Similarity 34.6%; Pred. No. 1.7e-49; 7;
 Matches 128; Conservative 57; Missmatches 109; Indels 76; Gaps 7;
 Db 1 MGIYLCSPKTDKTSEDDENAEELRYGLSAMQWRDSSMEDAHKAIIANVDKNTST-SIIFGIFD 59
 Db 1 MGAFLDKPKTEKHNAHAGANGLRYGLSSMQGWRVEMEDAHTAVVGGIPHGLEDWSFFAVYD 60
 Qy 60 GHGKKLVAKFCAKHLHQEVLKSEAY-AKGDLIKASLEY S-----FLRMDDEMMKGA 107
 Db 61 GHAGSRVANYCSTHLLHITTNEDFRAAGKSGSALELSVENVKNGIRTGFKLKIDEMRNF 120
 Qy 108 SGWKELOQSLEETSSQLDKLGNGNNSSSNAREDDESDES DSYAVLTTESSNDSNLATRKHKYSDFQ 167
 Db 121 S-----DLRNGMDRS-----130
 Qy 168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRGEAVNLSTDHKPNLEHERKRRIESAGGF 227
 Db 131 ----GSTAVGYMISPKHIYFINCGDSRAVLYRNQVCFSQTQDHKPNCNPREKERIONAGGS 186
 Qy 228 VHGGRVNGSLNLTRAI GDMEFKGRPDLPDKQVVTCCPDVVEVLGPDEFIVLACDGIW 287
 Db 187 VMIQRVNGLS LAVSRLAQLGDYKCVDGKGPTEQLVSPEPEVYELLRAEEDFILACDGIW 246
 Qy 288 DVMSQAVVDFVKSRLPPTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIV---QPKQ 343
 Db 247 DVMSENELCEYVKSRLLEVSDDILENVCNWWVDTCLHKGSR-----DNMSIVLWCFSNAPKV 301
 Qy 344 SGVAASSSTD 353
 Db 302 SDEAVRKDSE 311

RESULT 4
 US-08-873-093-4
 Sequence 4, Application US/08873093
 Patent No. 5853997
 GENERAL INFORMATION:
 APPLICANT: Bandman, Olga
 APPLICANT: Goli, Surya K.
 APPLICANT: Lal, Preeti
 APPLICANT: Corley, Neil C.
 APPLICANT: Zhang, Hong
 TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE

Qy 288 DVMSQAVVDFVKSRLPPTKTLSSLCEEILDYCLSPTTRQQEGCDNMSIIIV---QPKQ 343
 Db 247 DVMSENELCEYVKSRLLEVSDDILENVCNWWVDTCLHKGSR-----DNMSIVLWCFSNAPKV 301
 Qy 344 SGVAASSSTD 353
 Db 302 SDEAVRKDSE 311

RESULT 5
 US-08-873-093-3

Sequence 3, Application US/08873093
 Patent No. 5853997
 GENERAL INFORMATION:
 APPLICANT: Bandman, Olga
 APPLICANT: Goli, Surya K.
 APPLICANT: Lal, Presti
 APPLICANT: Corley, Neil C.
 APPLICANT: Zhang, Hong
 TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3114 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/873,093
 FILING DATE: Filed Herewith
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0319 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-845-4166
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 390 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 1247927
 US-08-873-093-3

Query Match 29.1%; Score 534; DB 2; Length 390;
 Best Local Similarity 34.3%; Pred. No. 3.3e-49;
 Matches 125; Conservative 54; Mismatches 109; Indels 76; Gaps 6;

QY 1 MGIYLCSPTKTDKTSEDDENAEELRYGLSAMQGWRDSDMEDIKAHLHQEVLKSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 107
 DB 1 MGAFLDKPKTEKHNAAHGAGNGLRGYGLSSMQGWRVEMEDIAHTAVVGIPHGLEDWSSFFAVYD 60

QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 107
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGFALEPSVENVKTGIRTGFLKIDEYMRNF 120

QY 108 SGWKELQSLEETSSQLDKLGNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 167
 DB 121 S-----DLRNGMDRS-----130

QY 168 GPIYGSTAVVALIRGNKLIFVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGF 227
 DB 131 ---GSTAVGVMISPTHIYFINCGDSRAVLCRNGQVCFCSTQDHKPNCNPMEKERIONAGGS 186

QY 228 VHGGGRVNGSLNLTRAIQDMEEFKGRPDLPPDRQVVTCCPDVVEVLGPGDEFIVLACDGIW 287
 DB 187 VMIQRVNGLSLAVSRAILGDXYKCVDGKGPTEQLYSPEPEVYEILRAEEDDEFVVLACDGIW 246

QY 288 DVMSQAOAVDFVKSRPLPTKTLSSLCEIIIDYCLSPTTRQQECDMSIIIV---QPKQ 343
 QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

Db 247 DVMSNEELCEFVNSRLEVSSDDLENVCNWVVDTCLHKGSR----DNMSIVLVCFANAPKV 301
 QY 344 SGVA 347
 Db 302 SDEA 305

RESULT 6
 US-08-822-701-7 ; Sequence 7, Application US/08822701
 ; Patent No. 5976853
 ; GENERAL INFORMATION:
 ; APPLICANT: Guttridge, Mark
 ; APPLICANT: Basilio, Claudio
 ; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
 ; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David A. Jackson, Esq.
 ; STREET: 411 Hackensack Ave, Continental Plaza, 4th
 ; STREET: Floor
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/822,701
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1049-1-002 N
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 309 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 US-08-822-701-7
 ORGANISM: Mus musculus
 Query Match 29.1%; Score 533.5; DB 2; Length 309;
 Best Local Similarity 34.7%; Pred. No. 2.6e-49;
 Matches 125; Conservative 56; Mismatches 104; Indels 75; Gaps 7;

QY 1 MGIYLCSPTKTDKTSEDDENAEELRYGLSAMQGWRDSDMEDIKAHLHQEVLKSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 1 MGAFLDKPKTEKHNAAHGAGNGLRGYGLSSMQGWRVEMEDIAHTAVVGIPHGLEDWSSFFAVYD 60

QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

QY 109 GWKELQSLEETSSOLDKLGNNGNSSSNAREDDESDYSYAVLTESNDNLATKKHKYSDFQ 168
 QY 60 GHGGKLVAKEFCAKHLHQEVLRSEAYAKGD-----LKASLEYSLFLRMDEMMKGA 108
 DB 61 GHAGSRVANYCSTHLLEHITTNEDFRAADKGSALEPSVSVKTGRTGFLKIDEYMRNF 120

QY 121 -----121

QY 169 PIYGSTAVVALIRGNKLFLVANAGDSRCIMSRGAEVNLSIDHKPNLEHERKRIESAGGFV 228

Q

Db 130 ---GSTAVGYMVSPTHMYFINGDSRAVLCRNGQVCFSTQDHKPCNPVEKERIONAGGSV 186 Db 121 -----DLRNGMDRS-----

Qy 229 HGGRVNGSLNLTRAIGDMEFKGRPDQLPPDKDQVVTCCPDPVVYVDLGPGEDEFIVLACDGIVD 288 Qy 169 PIYGSTAVVALIRGNKLEVANAGDSRCIMSRGEAVNLSDIDHKPNLEHERKRIESAGGFV 228

Db 187 MIQRVNGSLAVSRAALGDYDVKCVDGKGPTEQLVSPEPEVYEIVRAAEEDEFVVLACDGIVD 246 Db 130 ---GSTAVGVMSVSPTHMFINGDSRAVLCRNGQVCFSTQDHKPCNPVEKERIONAGGSV 186

Qy 289 VMSSQAVDFVKSRLPPTKTLSSLCEEILDYCLSPTRQQEGCDNMSIIIV---QPKQS 344 Qy 229 HGGRVNGSLNLTRAIGDMEFKGRPDQLPPDKDQVVTCCPDPVVYVDLGPGEDEFIVLACDGIVD 288

Db 247 VMSNEELCEFVKSRLFEVSDDLENVCNWVVDTCLHKGSR----DNMSVVLVCFSNAPKVS 301 Db 187 MIQRVNGSLAVSRALGDDYKVDGKGPTEQLVSPEPEVYEIVRAEEDDEFVVLACDGIVD 246

RESULT 7 ; Sequence 7, Application US/08935855

US-08-935-855-7 ; Sequence 7, Application US/08935855

GENERAL INFORMATION:

APPLICANT: Guthridge, Mark ; Sequence 8, Application US/08822701

Patent No. 6066485 ; Patent No. 5976853

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq. ; GENERAL INFORMATION:

STREET: 411 Hackensack Ave, Continental Plaza, 4th ; APPLICANT: Basilico, Claudio

STREET: Floor ; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE

CITY: Hackensack ; NUMBER OF SEQUENCES: 22

STATE: New Jersey ; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13

ZIP: 07601 ; NUMBER OF SEQUENCES: 22

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible ; NUMBER OF SEQUENCES: 22

OPERATING SYSTEM: PC-DOS/MS-DOS ; NUMBER OF SEQUENCES: 22

SOFTWARE: Patent In Release #1.0, Version #1.30 ; NUMBER OF SEQUENCES: 22

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/935,855 ; NUMBER OF SEQUENCES: 22

FILING DATE:

CLASSIFICATION: 435 ; NUMBER OF SEQUENCES: 22

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A. ; NUMBER OF SEQUENCES: 22

REGISTRATION NUMBER: 26,742 ; NUMBER OF SEQUENCES: 22

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800 ; NUMBER OF SEQUENCES: 22

TELEFAX: 201-343-1684 ; NUMBER OF SEQUENCES: 22

INFORMATION FOR SEQ ID NO: 7 :

SEQUENCE CHARACTERISTICS:

TYPE: amino acid ; LENGTH: 309 amino acids

STRANDEDNESS: single ; TOPOLogy: linear

MOLECULE TYPE: protein ; HYPOTHETICAL: NO

HYPOTHETICAL: NO ; FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM: Mus musculus ; NUMBER OF SEQUENCES: 22

US-08-935-855-7 ; NUMBER OF SEQUENCES: 22

Query Match 29.1%; Score 533.5; DB 3; Length 309; ; ORIGINAL SOURCE: Rattus

Best Local Similarity 34.7%; Pred. No. 2.6e-49; ; ORGANISM: Rattus

Matches 125; Conservative 56; Missmatches 104; ; FRAGMENT TYPE: NO

Gaps 7; ; NUMBER OF SEQUENCES: 22

Query Match 28.3%; Score 520; DB 2; Length 306; ; NUMBER OF SEQUENCES: 22

Best Local Similarity 34.6%; Pred. No. 7.3e-48; ; NUMBER OF SEQUENCES: 22

Matches 125; Conservative 58; Missmatches 104; ; NUMBER OF SEQUENCES: 22

Gaps 9; ; NUMBER OF SEQUENCES: 22

Qy 1 MGIYLCSPTKTDKTSEDDENAEILRYGLSAMOGWRDSMEDAHKAIIIVDKNTST-SIFGIFD 59 Qy 1 MGIYLCSPTKTDKTSEDDENAEILRYGLSAMOGWRDSMEDAHKAIIIVDKNTST-SIFGIFD 59

Db 1 MGAFLDKPKTEKHNAHAGANGLRYGLSSMQGWRVEMEDAHTAVVGGIPHGLDNWSFFAVYD 60 Db 1 MGAFLDKPKMEKHNAAQGQGNGLRYGLSSMQGWRVEMEDAHTAVVGLPSGLETWSSFAVYD 60

Qy 60 GHGGKLVAKECAKHLHQEVLKSEAYAKD----LKASLE----YSFLRMDEMKGAS 108 Qy 1 MGIVLCSPTKTDKTSEDDENAEILRYGLSAMOGWRDSMEDAHKAIIIVDKNTST-SIFGIFD 59

Db 61 GHAGSRWANYCSTHLLEHITTNEDEAADSNSALEPSVESVKTGRTGFLKIDEYMRNFs 120 Db 1 MGIVLCSPTKTDKTSEDDENAEILRYGLSAMOGWRDSMEDAHKAIIIVDKNTST-SIFGIFD 59

Qy 109 GWKELQSLEETSSQLDKLGNGNSSNAREDDESDSSYAVLTESNDSNLTAKKKHYSDFQG 168 Qy 60 GHGGKLVAKECAKHLHQEVLKSEAYAKG----DLKASLEYSFLRMDEMKGASGWK 111

Db 61 GHAGSQVAKYCCEHLLDHITNNQDF-KGSAGAPSVENVKNGIRTGFLEIDEHMR----- 113
 Qy 112 ELQSLEETSSQLDKLGNNSSSNAREDDDESYSAYVLTESNDSNLATKKHHKYSDFQGPIY 171
 Db 114 -----KKH-----VMSE-----GADRS 125
 Qy 172 GSTAVVALIRGNKLTVANAGDSRCIMSRGGAEVNLSIDHKPNLEHERKRIESAGGFVHGG 231
 Db 126 GSTAVGVLIISPOQHTYFINGDSRGILLCRNRKVHFFTDHKPSNPLERIQNAGGSVMIQ 185
 Qy 232 RVNGSLNLNTRAIQDMEEFKGRPDLPDKQVVTCCPDVVEVDLG-PGDEFIVLACDGIWDM 290
 Db 186 RVNGSLAVSRLALGDFDYKCVHKGKPTEQVSPPEVHDIERSEEDQFILACDGIWDM 245
 Qy 291 SSQAVVDFVKSRLPTKTLSSLCEEILDYCLSPTTRQEGCDNMSIIIV---QPKQSGV 346
 Db 246 GNEELCDFVRSLRLEYTDDLEKVCNEVVDTCLYKGSR----DNMSVILICFPNAPKVSAE 300
 Qy 347 A 347
 Db 301 A 301

RESULT 9
 US-08-935-855-8
 Sequence 8, Application US/08935855
 Patent No. 6066485

GENERAL INFORMATION:
 APPLICANT: Guthridge, Mark
 APPLICANT: Basilico, Claudio
 TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE SERINE/THREONINE PHOSPHATASE, FIN13
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/935,855
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 306 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 HYPOTHETICAL: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 ORGANISM: Rattus
 US -08-935-855-8

Matches 125; Conservative 58; Mismatches 104; Indels 74; Gaps 9;
 Qy 1 MGIVLCSPKTDKTSEDDENAEILRYGLSAMQGWRDMSMEDAHKAIALNVDKNTST-SIFGIFD 59
 Db 1 MGAFLDKPKMEKHNAQGQGNGLRYGLSSMQGWRVEMEDAHTAVIGLPSGLETSWSFFAVYD 60
 Qy 60 GHGGKLVAKFCAKHLHQEVLKSEAYAKG-----DLKASLEYSLFRMDEMKGASGWK 111
 Db 61 GHAGSQVAKYCCEHLLDHITNNQDF-KGSAGAPSVENVKNGIRTGFLEIDEHMR---- 113
 Qy 112 ELQSLEETSSQLDKLGNNSSSNAREDDDESYSAYVLTESNDSNLATKKHHKYSDFQGPIY 171
 Db 114 -----KKH-----VMSE-----GADRS 125
 Qy 172 GSTAVVALIRGNKLTVANAGDSRCIMSRGGAEVNLSIDHKPNLEHERKRIESAGGFVHGG 231
 Db 126 GSTAVGVLIISPOQHTYFINGDSRGILLCRNRKVHFFTDHKPSNPLEKERIQNAGGSVMIQ 185
 Qy 232 RVNGSLNLNTRAIQDMEEFKGRPDLPDKQVVTCCPDVVEVDLG-PGDEFIVLACDGIWDM 290
 Db 126 GSTAVGVLIISPOQHTYFINGDSRGILLCRNRKVHFFTDHKPSNPLEKERIQNAGGSVMIQ 185
 Qy 291 SSQAVVDFVKSRLPTKTLSSLCEEILDYCLSPTTRQEGCDNMSIIIV---QPKQSGV 346
 Db 246 GNEELCDFVRSLRLEYTDDLEKVCNEVVDTCLYKGSR----DNMSVILICFPNAPKVSAE 300
 Qy 347 A 347
 Db 301 A 301

RESULT 10
 US-08-822-701-2
 Sequence 2, Application US/08822701
 Patent No. 5976853
 GENERAL INFORMATION:
 APPLICANT: Guthridge, Mark
 APPLICANT: Basilico, Claudio
 TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE SERINE/THREONINE PHOSPHATASE, FIN13
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/822,701
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1049-1-002 N
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 306 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 HYPOTHETICAL: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 ORGANISM: Rattus
 US -08-935-855-8

Query Match 28.3%; Score 520; DB 3; Length 306;
 Best Local Similarity 34.6%; Pred. No. 7.3e-48;

; FRAGMENT TYPE: N-terminal
 US-08-822-701-2

Query Match 26.8%; Score 491.5; DB 2; Length 392;
 Best Local Similarity 46.0%; Pred. No. 1.3e-4;
 Matches 109; Conservative 44; Mismatches 73; Indels 11; Gaps 5;

Qy 112 ELQSLEETSSQLDKLGNNSNSNA-REDDDESDSAVALTEESNDNLATKKHYSDFQGPI 170
 Db 116 EVEEEEDDSEECECSEDEDGYSSEAENEEDDEDDTEEA-EEDDDEEMVPGMEGKEPGSD 173

Qy 112 ELQSLEETSSQLDKLGNNSNSNA-REDDDESDSAVALTEESNDNLATKKHYSDFQGPI 170
 Db 116 EVEEEEDDSEECECSEDEDGYSSEAENEEDDEDDTEEA-EEDDDEEMVPGMEGKEPGSD 173

Qy 112 ELQSLEETSSQLDKLGNNSNSNA-REDDDESDSAVALTEESNDNLATKKHYSDFQGPI 170
 Db 116 EVEEEEDDSEECECSEDEDGYSSEAENEEDDEDDTEEA-EEDDDEEMVPGMEGKEPGSD 173

Qy 171 YGSTAVVALIRGNKLFVANAGDSRCIMSRGEAVNLSIDHKPNEHERKRIESAGGGFV-H 229
 Db 174 SGTTAVVALIRGKQLIVANAGDSRCVVSSEAGKALDMSYDHKPEDVELARIKNAGGKVTM 233

Qy 171 YGSTAVVALIRGNKLFVANAGDSRCIMSRGEAVNLSIDHKPNEHERKRIESAGGGFV-H 229
 Db 174 SGTTAVVALIRGKQLIVANAGDSRCVVSSEAGKALDMSYDHKPEDVELARIKNAGGKVTM 233

Qy 230 GGRVNGSLNLTRAIQDMFGRPDLPDPDKQVVTCCPDDVVEVDLGPGEDEFIVLACDGIVWDV 289
 Db 234 DGRVNGGLNLNSRAIGDHFYKRNKNLPPQEQMISALPDIVKLTIDDHREFMVIACDGIWNV 293

Qy 230 GGRVNGSLNLTRAIQDMFGRPDLPDPDKQVVTCCPDDVVEVDLGPGEDEFIVLACDGIVWDV 289
 Db 234 DGRVNGGLNLNSRAIGDHFYKRNKNLPPQEQMISALPDIVKLTIDDHREFMVIACDGIWNV 293

RESULT 12
 US-09-013-881-2
 ; Sequence 2, Application US/09013881
 ; Patent No. 6132964

GENERAL INFORMATION:

APPLICANT: Bandman, Olga
 APPLICANT: LaL, Preeti
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Corley, Neil C.
 APPLICANT: Guegler, Karl J.
 APPLICANT: Shah, Purvi

TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
 NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/013,881
 FILING DATE: HEREWITH
 CLASSIFICATION:
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/013,881
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esg., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: PF-0470 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 392 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 FRAGMENT TYPE: N-terminal

Query Match 26.8%; Score 491.5; DB 3; Length 392;
 Best Local Similarity 46.0%; Pred. No. 1.3e-4;

Query Match 20.28%; Score 370.5; DB 4; Length 392;
 Best Local Similarity 28.0%; Pred. No. 1.6e-31;

US-09-013-881-2

Matches 106; Conservative 60; Mismatches 94; Indels 119; Gaps 12; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Saccharomyces cerevisiae
; US-08-822-701-9

Query Match 18.6%; Score 341.5; DB 2; Length 281;
; Best Local Similarity 28.0%; Pred. No. 1.3e-28;
; Matches 96; Conservative 52; Mismatches 110; Indels 85; Gaps 11;

Query 14 SEDDENAELRYGLSAMQG-----WRDSMEDAHKATLNVDKNTSTSIFGIFDGHGGKL 65
; Db 5 SEILERPETPYDITYRVGAENKNSKFRRTMEDVHTYYKNFASRLDWGYFAVEDGHAGIQ 64

Query 66 VAKFCAKHLH----QEVLKSEAYAKGDLKASLEYSLFLR 99
; Db 65 ASKWCGKHLHTIEQNILADET---RDVRDVNLNDSLAID-
; 106

Query 122 QLDKLGNNGNSSSNAREDDDESDSYAVL----TESNSNLATKKHKYSDFQGPPIYGSTAV 121
; Db 107 KL---VGNSGCTA-----AVCVLRWELPDVSDDSMMDLAQHQ----
; 140

Query 177 VALIRGNKLFVANAGDSRCIMSRGEAVNLSDHKPNLEHERKRIESAGGFVHGGRVNGS 236
; Db 141 -----RKLYTANVGDSRIVLFRNGNSIRLTYDHKASDTLEMORVEQAGGLIMKSRRVNGM 194

Query 237 LNLTRAIGDMEEFKGRDLPDKQVVTCCPDPVVEDLGPGDEFIVLACDGIWDMSSQAVV 296
; Db 195 LAVTRSLGDKFF-----DSLVYGSPPFTTSVEITSEDKFLILACGLWDVIDDDQDAC 245

Query 297 DFVKSRRLPTTKTLSSLCEEILDYCLSPPTTRQEGCDNMSIIIV 339
; Db 246 ELIKDITEPNEAAKVLVRYALE---NGTT----DNVTVMVV 279

RESULT 13
; Sequence 9, Application US/08822701
; Patent No. 5976853

GENERAL INFORMATION:

APPLICANT: Guthridge, Mark
; APPLICANT: Basilico, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor 22
; CITY: Hackensack
; STATE: New Jersey
; ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/822,701
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; LENGTH: 281 amino acids
; TYPE: amino acid

RESULT 14
US-08-935-855-9
; Sequence 9, Application US/08935855
; Patent No. 6066485
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basilico, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; ZIP: 07601
; CURRENT APPLICATION DATA:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/935,855
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; LENGTH: 281 amino acids
; TYPE: amino acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 ORGANISM: *Saccharomyces cerevisiae*
 US-08-935-855-9

Query Match 18.6%; Score 341.5; DB 3; Length 281;
 Best Local Similarity 28.0%; Pred. No. 1.3e-28;
 Matches 96; Conservative 52; Mismatches 110; Indels 85; Gaps 11;

Query Match 17.8%; Score 326; DB 2; Length 314;
 Best Local Similarity 30.2%; Pred. No. 7.2e-27;
 Matches 109; Conservative 48; Mismatches 120; Indels 84; Gaps 12;

Query Match 17.0%; Score 314; DB 1; Length 314;
 Best Local Similarity 30.2%; Pred. No. 7.2e-27;
 Matches 109; Conservative 48; Mismatches 120; Indels 84; Gaps 12;

Qy 14 SEDDENAEALRYGLSAMQG-----WRDSMEDDAHKAILNVDKNTSTSIFGIFDGGKKL 65
 Db 5 SEILERPETPYDITYRVGVAENKNSKFRRTMEDVHTYVKNEASRLDWGYFAVFDGHAGIQ 64

Qy 66 VAKFCAKHLH----QEVLKSEAYAKGDLKASLEYSFLRMDEMKGASGWKELOSLEETS 121
 Db 65 ASKWCGRHLHTIEQNILADET---RDVDRVLNDSFLAID-----EEINT 106

Qy 122 QLDKLGNGNSSSNAREDDDESDDSYAVL----TESNDSNLATKKHYSDFQGPPIYGSTAV 176
 Db 107 KL----VGNSGCTA----AVCYLRLWELPDVSDDSMQLAQHQ-----140

Qy 177 VALIRGNKLFYANAGDSRCIMSRGEAVNLSDHKPNEHERKRIESAGGFVHGRVNGS 236
 Db 141 -----RKLYTANVGDSRIVLFRNGNSIRLTYDHKASDTLEMQRVEQAGGLIMKSRVNGM 194

Qy 237 LNLTRAIQDMEEFKGRPDLPDKQQVVTCCPDVVEDLGPDEFIVLACDGIWDMSSQAVV 296
 Db 195 LAVTRSLGDKFF----DSLVVGSPPFTTSVETSEDKFLILACDGLWVDVIDDDQDAC 245

Qy 297 DFVKSRLPTTKTLSSLCEIILYCLSPTTROEQGCNDMSLIV 339
 Db 246 ELIKDITEPNEAAKVLVRYALE--NGTT----DNVTVMVV 279

RESULT 15
 US-08-822-701-10
 Sequence 10, Application US/08822701
 Patent No. 5976853

GENERAL INFORMATION:
 APPLICANT: Guthridge, Mark
 ADDRESS: Basilico, Claudio
 TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCTIBLE
 TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 STREET: Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/822,701
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1049-1-002 N
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEXFAX: 201-343-1684



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Human MP-19 full	546	19	AAW80287
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Drosophila melanog	367	22	ABB62019
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Human protein phos	479	20	AAW94283
Human secreted pro	387	21	AY86261
Human prostate can	400	21	AAB56676
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FIN13 serine/threo	392	18	AAG30091
Arabidopsis thalia	182	21	AAG08499
zea mays protein f	149	21	AAG41163
Arabidopsis thalia	175	21	AAG08500
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zea mays protein f	253	21	AAG34224
A. thaliana enviro	380	21	AAY77963
Human polypeptide	392	22	AAM38769
Human protein sequ	392	22	AAB92585
Human hydrolase-li	392	22	AAB28791
Human protein phos	421	22	ABB12317
Human polypeptide	421	22	AAM40555
Novel human enzyme	441	22	AAU23566
Novel human enzyme	446	22	AAU22933
zea mays protein f	114	21	AAG41054
Arabidopsis thalia	354	21	AAG06997
Arabidopsis thalia	423	22	AAE01345
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ALIGNMENTS

RESULT 1	1	AAG43237
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KW		Protein identification; signal transduction pathway; metabolic pathway;
KW		hybridisation assay; genetic mapping; gene expression control; promoter;
KW		termination sequence.
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OS		Arabidopsis thaliana.
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PN		EP1033405-A2.
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PD		06-SEP-2000.
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PF		25-FEB-2000; 2000EP-0301439.

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	869	47.3	327	AAG43888
4	866	47.2	329	AAG43238
5	838	45.6	320	AAG43889
6	832	45.3	322	AAG43239
7	764	41.6	315	AAG11786
8	764	41.6	336	AAG11785
9	764	41.6	339	AAG11784
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 XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 54908.
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DT	18-OCT-2000	(first entry)	
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 XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX Arabidopsis thaliana.
 OS Arabidopsis thaliana.
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Qy 89 LKASLEYSLFLRMDEMMSKGASGWKELQSLEETSSQLDKLGN-----NSSSNAREDESDY 143
 Db 59 vgtslqkafffrmdeinqqrgwrelavlgdkinkfsgmiegliwspsgdsankpkda--- 115

Qy 144 SYAVLSESSNDNSNLATRKHKYSDFQGPIYGSTAVVALIRGNKLFVANAGDSRCIIMSRGEA 203
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Qy 204 VNLSIDHKPNLEHERKRITESAGGGFVHGRVNGSLNLTTRAIGDMEFKGRPDLPDKQVVTC 263
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QY	156 LATKKHKYSDFQGPPIYGSTAVVALLIRGNKLFLVANAGDSRCIMSSRRGEAVNLSIDHKPNLE 215	45.6%; Score 838; DB 21; Length 320;
Db	109 wp ledgphsdftgptsgctacvalikdkkk1fvanagdsrcvisrkssqaynlsskdhkpdle 168	Matches 164; Conservative 55; Mismatches 87; Indels 12; Gaps 2;
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QY	276 DEFIVLACDGIIWDVMSQSAVYDFVKSRLPPTKYLSSLCPTTROQEGLDNMS 335	45.6%; Score 838; DB 21; Length 320;
Db	229 ddf1vvacdgiwdcmssqelvdflieqlksetklistvcekvdrclapdtatgegcdnmt 288	Matches 164; Conservative 55; Mismatches 87; Indels 12; Gaps 2;
QY	336 IIIIVQPKOSGVAAASSSTD 353	45.6%; Score 838; DB 21; Length 320;
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KW hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

KW KW

XX OS Arabidopsis thaliana.

XX XX

PR EP1033405-A2.

XX XX

PR 06-SEP-2000.

XX XX

PR 25-FEB-2000; 2000EP-0301439.

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PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

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XX 17-OCT-2000 (first entry)

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XX KW Protein identification; signal transduction pathway; metabolic pathway;

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PR	18-AUG-1999;	99US-0149426.			
PR	20-AUG-1999;	99US-0149722.			
PR	20-AUG-1999;	99US-0149723.			
PR	20-AUG-1999;	99US-0149929.			
PR	23-AUG-1999;	99US-0149902.			
PR	23-AUG-1999;	99US-0149930.			
PR	25-AUG-1999;	99US-0150566.			
PR	26-AUG-1999;	99US-0150884.			
PR	27-AUG-1999;	99US-0151065.			
PR	27-AUG-1999;	99US-0151080.			
PR	30-AUG-1999;	99US-0151303.			
PR	31-AUG-1999;	99US-0151438.			
PR	01-SEP-1999;	99US-0151930.			

RESULT 10
AAB82980

Query Match	4.1.6%	Score 764;	DB 21;	Length 339;
Best Local Similarity	50.98;	Pred. No. 1.8e-62;	Mismatches	1;
Matches 149; Conservative	51;	Mismatches	83;	Indels 10; Gaps 1;
QY	61	HGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSLFRMDEMKGASGWKELQSLEETS 120	Db	43 hgqkvvakfcakyhqqvisneayktgdvetsrraffrmddmmqgqrwrelavlgdkm 102
QY	121	SQLDKLGNGNSSSNAREDDESDYSYAVLTESNDSNLATKKHKEYSDFGPIYGSTAVVALLI 180	Db	103 nkfsgmiegfiwsprsgd-----tnnqpdswnpledphsdfgtptsgctacvali 152
QY	181	RGNKLFVANAGDSRC1MSRGEAVNLSIDHKPNLEHERKRIBESAGGFVHGRVNGSLNLT 240	Db	153 kdkklfvanagdsrccvisrksqaynskdhkpdeleverkerilkaggfihagringslnlt 212
QY	241	RAIGDMEEFKGRPDQLPPDKQVVTCPCDVVEVDLGPGDEFIVLACDGIVWDGMSSQAVVDFVK 300	Db	213 raigdmefkqnkfplpsekqmvtadpdintidlcddaflvvacdgivwdcmssqelvdfin 272
QY	301	SRLPTTKTLSLCBEILYCLSPTRQEQEGDNMSIIIVQPQSGVAASSSTD 353	Db	273 eqlksetklistvcekvdrclapdtatgegcdnmtiilvqfknpnseteped 325

PS Claim 8; Page 12; 15pp; English.

XX The present sequence represents full length human MP-19, which
 CC is a serine/threonine phosphatase derived from human placenta. The
 CC nucleic acid sequence encodes a human protein phosphatase of the
 CC protein serine/threonine phosphatase family and is of the PP2C class
 CC which are regulate in the regulation of fatty acid and cholesterol
 CC biosynthesis. The MP-19 protein is useful in the treatment of leukaemia,
 CC brain, prostate and breast cancer, Alzheimer's, Huntington's or
 CC Parkinson's diseases, epilepsy, reproductive disorders and regulation of
 CC spermatogenesis or maturation of mammalian germ cells.

XX

QY 119 nfvdaeedlaelqeensnlplnevleykg1pqqkkldlkssdhkenfkmrspfyf 178
 QY 122 -----QLDKLGNNGNNSSN----- 134
 QY 179 rgrraaalaaeattnkavmdpsakpdgssstsaaaaalsadgvansrpsnvnpmagad 238
 DB 135 -----AREDDE-----SDYSYAVLTERNSNDNLAT----- 158
 QY 239 snttsindlstknaalkddsvndqnegsngtdfkhtlvssnnkkfatgsndmtelnqs 298
 DB 159 RKHKY-----SDFQ----- 167
 QY 299 skeftnsstskeferninsqqdeftdddadyeendnvkspdtsaessdctenddaggd 358
 DB 168 -----GPIYGSTAVVALIRGNKLFVANAGDSRCIM 197
 QY 359 edgnedsdeetdedqmandnfcanmieepgkdsgctavcvclqgrdllyvanagdsrcvi 418
 QY 198 SRRGEAVNLSIDHKPNLEHERKRIESAGGFVH-GGRVNNGSLNLTRAIGDMERFKGRPDLP 256
 DB 419 srsgqaiemsidhkpeddeeasriikaggrvrtldgrvnnglqlsralgdhayktntlp 478
 QY 257 DKQVVTCACPDPVVEVDLGPDEFIFVLACDGIIWDWMSQAVDFVKSRLPPTKTLSSLCEII 316
 DB 479 eeqmisalpdiikkliitpedfmvlacdgiwnymsseevfvrclkdnnkklisticei 538
 QY 317 LDYCLSPPTTR-QQECCDNMSIIIVQPK-----QSGVAASSSTD 353
 DB 539 fdnclapntmgdqcdnmtnavivqfkqkklqelqstippnqted 582
 QY 540 -----QSLEETSSQLD-----KLGNNGNNSSNAR----- 136
 DB 179 eepgssqqlngaeagpedstrtpsqengptkaytgfssnserteaagqvgepgipgtgeag 238
 QY 114 -----EDDES DSYAVLTERNSNDNLATKKHYSDFQ----- 167
 DB 179 eepgssqqlngaeagpedstrtpsqengptkaytgfssnserteaagqvgepgipgtgeag 238
 QY 137 -----EDDES DSYAVLTERNSNDNLATKKHYSDFQ----- 167
 DB 239 pscssasdklprvakskffedsedesdeaaeeeeseedgysseeaeneedddt 298
 QY 168 -----GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRRG 202
 DB 299 eeaeedeeeeeemvpgmegkeepgsdsqttavvalirgkqlivanagdsrvseagk 358
 QY 203 AVNLSIDHKPNLEHERKRIESAGGFV-HGGRVNNGSLNLTRAIGDMEFKGRPDLPDKQVV 261
 DB 359 aldmisydhkpedevelariknqgkvtnmdgrvnnglqlsraiqdhfykrknknlppeeqmi 418
 QY 262 TCCPDVVEVDLGPDEFIFVLACDGIIWDVMSQAVVDFVKSRLP-----TTKTLSSLC 315
 DB 419 salpdikvitltdhefmviacdgiwnvmsseqvdifqskisqrdenelrllissive 478
 QY 316 ILDYCLSP-TTROQEGCDNMSIIIRV 339
 DB 479 11dqcldaptsgdgtgcdnmntcii 503
 QY 320 -----RESULT 13
 ID AAG55036
 DT 18-OCT-2000 (first entry)
 QY 321 Human MP-19 full length protein sequence.
 QY 322 Human; MP-19; serine-threonine phosphatase; cancer; diagnosis;
 KW phosphorylation dependent disease; leukaemia; breast; brain;
 prostate; epilepsy; fatty acid; cholesterol.
 Homo sapiens.
 QY 323 Key Location/Qualifiers
 Region 1..112
 /note= "protein sequence given in the specification"
 Region 1..546
 /note= "protein decoded by AAV66512"
 EP874052-A2.
 PN 28-OCT-1998.
 PD 22-APR-1998; 98EP-0107346.
 PR 22-APR-1997; 97EP-0106658.
 PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEM ENTWICKL.
 XX Hanke M, Paulista M, Pohl J;
 PI WPI; 1998-544644/47.
 XX N-PSDB; AAV66512.
 PT DNA encoding human protein phosphatase polypeptide - useful in
 treatment of leukaemia, breast, brain and prostate cancer, epilepsy
 etc.

XX 06-SEP-2000. PR 02-JUL-1999; 99US-0142055.
 PD 25-FEB-2000; 2000EP-0301439. PR 06-JUL-1999;
 XX PR 08-JUL-1999; 99US-0142390.
 PR 05-MAR-1999; 99US-0123180. PR 09-JUL-1999;
 PR 09-MAR-1999; 99US-0123548. PR 08-JUL-1999;
 PR 23-MAR-1999; 99US-0125788. PR 12-JUL-1999;
 PR 25-MAR-1999; 99US-0126264. PR 13-JUL-1999;
 PR 29-MAR-1999; 99US-0126785. PR 14-JUL-1999;
 PR 01-APR-1999; 99US-0127462. PR 15-JUL-1999;
 PR 06-APR-1999; 99US-0128234. PR 16-JUL-1999;
 PR 08-APR-1999; 99US-0128714. PR 17-JUL-1999;
 PR 16-APR-1999; 99US-0129845. PR 18-JUL-1999;
 PR 19-APR-1999; 99US-0130077. PR 19-JUL-1999;
 PR 21-APR-1999; 99US-0130449. PR 20-JUL-1999;
 PR 23-APR-1999; 99US-0130510. PR 20-JUL-1999;
 PR 23-APR-1999; 99US-0130891. PR 19-JUL-1999;
 PR 28-APR-1999; 99US-0131449. PR 19-JUL-1999;
 PR 30-APR-1999; 99US-0132048. PR 19-JUL-1999;
 PR 30-APR-1999; 99US-0132407. PR 20-JUL-1999;
 PR 04-MAY-1999; 99US-0132484. PR 20-JUL-1999;
 PR 05-MAY-1999; 99US-0132485. PR 21-JUL-1999;
 PR 06-MAY-1999; 99US-0132486. PR 21-JUL-1999;
 PR 06-MAY-1999; 99US-0132487. PR 21-JUL-1999;
 PR 07-MAY-1999; 99US-0132863. PR 21-JUL-1999;
 PR 11-MAY-1999; 99US-0134256. PR 22-JUL-1999;
 PR 14-MAY-1999; 99US-0134218. PR 22-JUL-1999;
 PR 14-MAY-1999; 99US-0134219. PR 22-JUL-1999;
 PR 14-MAY-1999; 99US-0134221. PR 23-JUL-1999;
 PR 14-MAY-1999; 99US-0134370. PR 23-JUL-1999;
 PR 18-MAY-1999; 99US-0134768. PR 23-JUL-1999;
 PR 19-MAY-1999; 99US-0134941. PR 23-JUL-1999;
 PR 20-MAY-1999; 99US-0135124. PR 23-JUL-1999;
 PR 21-MAY-1999; 99US-0135353. PR 23-JUL-1999;
 PR 24-MAY-1999; 99US-0135629. PR 24-JUL-1999;
 PR 03-JUN-1999; 99US-0136021. PR 03-AUG-1999;
 PR 04-JUN-1999; 99US-0136392. PR 04-AUG-1999;
 PR 07-JUN-1999; 99US-0136782. PR 07-JUL-1999;
 PR 08-JUN-1999; 99US-0138094. PR 08-JUL-1999;
 PR 10-JUN-1999; 99US-0138540. PR 10-JUL-1999;
 PR 10-JUN-1999; 99US-0138847. PR 10-AUG-1999;
 PR 14-JUN-1999; 99US-0139119. PR 11-AUG-1999;
 PR 16-JUN-1999; 99US-0139452. PR 12-AUG-1999;
 PR 18-JUN-1999; 99US-0139453. PR 13-AUG-1999;
 PR 18-JUN-1999; 99US-0139492. PR 13-AUG-1999;
 PR 18-JUN-1999; 99US-0139454. PR 16-AUG-1999;
 PR 18-JUN-1999; 99US-0139455. PR 17-AUG-1999;
 PR 18-JUN-1999; 99US-0139456. PR 18-AUG-1999;
 PR 18-JUN-1999; 99US-0139457. PR 20-AUG-1999;
 PR 18-JUN-1999; 99US-0139458. PR 20-AUG-1999;
 PR 18-JUN-1999; 99US-0139459. PR 23-AUG-1999;
 PR 18-JUN-1999; 99US-0139460. PR 23-AUG-1999;
 PR 18-JUN-1999; 99US-0139461. PR 23-AUG-1999;
 PR 21-JUN-1999; 99US-0139817. PR 25-AUG-1999;
 PR 22-JUN-1999; 99US-0139899. PR 30-AUG-1999;
 PR 23-JUN-1999; 99US-0140353. PR 31-AUG-1999;
 PR 23-JUN-1999; 99US-0140354. PR 01-SEP-1999;
 PR 24-JUN-1999; 99US-0140695. PR 07-SEP-1999;
 PR 28-JUN-1999; 99US-0140823. PR 10-SEP-1999;
 PR 29-JUN-1999; 99US-0140991. PR 13-SEP-1999;
 PR 30-JUN-1999; 99US-0141287. PR 15-SEP-1999;
 PR 01-JUL-1999; 99US-0141842. PR 16-SEP-1999;
 PR 01-JUL-1999; 99US-0142154. PR 20-SEP-1999;

PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160742.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
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 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
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 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 34.2%; Score 627; DB 21; Length 258;
 Best Local Similarity 49.2%; Pred. No. 6.4e-50;
 Matches 125; Conservative 43; Mismatches 76; Indels 10; Gaps 1;

QY 100 MDEMKGASGWKELOSLEETSSQDKLGNNGNNSSNAREDDDESVDYAVLTESNDNSNLATK 159
 ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 1 mddmmqgqrqwrelavlgdkmnkfsgmiegfiwsprsgd-----tnnqpdswwple 50

QY 160 KHKSDFEQPIYGSTAVVALIRGNKLFWANAGDSRCIMSRGEAVNLSTDHKPNLEHERK 219
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 Db 51 dgphsdfgtptsgctacvalikdkkfvanagdsrvclsqaynlkskdhkpdlieveke 110

QY 220 RIESAGGFVHGGRNGSLNLTRAIQDMEFFGRPDLPDKQVVTCCPDVVEVLGLPGDEFI 279
 |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 111 rilkaggfihaagringslnlraiqdmefkqnkfplsekqmvtaadpdintidcdddff 170

QY 280 VLA CDGIW DVM MSS QAV DFEVK SRL PTT KTL SS LCE ELL DY CLS PTT RQEG C DNMS LII Y 339
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 171 vvacdgiiwcdmssqelvdflheqlksetklstvcekvdrclapdtatgegdnmtiilv 230

QY 340 QPKQSGVAASSSTD 353
 ||:||:||:
 Db 231 qfk kpnp seteped 244

RESULT 14
 ID AAG08498 Standard; Protein: 210 AA.
 XX
 AC
 XX
 DT 17-OCT-2000 (first entry)
 XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 6060.
 XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX OS Arabidopsis thaliana.
 XX PN EP1033405-A2.
 XX PR 06-SEP-2000.
 XX PR 25-FEB-2000; 2000EP-0301439.
 XX PR 25-FEB-1999; 99US-0121825.
 XX PR 05-MAR-1999; 99US-0123180.
 XX PR 09-MAR-1999; 99US-0123548.
 XX PR 23-MAR-1999; 99US-0125788.
 XX PR 25-MAR-1999; 99US-0126264.
 XX PR 29-MAR-1999; 99US-0126785.
 XX PR 01-APR-1999; 99US-0127462.
 XX PR 06-APR-1999; 99US-0128234.
 XX PR 08-APR-1999; 99US-0128714.
 XX PR 16-APR-1999; 99US-0129845.
 XX PR 19-APR-1999; 99US-0130077.
 XX PR 21-APR-1999; 99US-0130449.
 XX PR 23-APR-1999; 99US-0130510.
 XX PR 23-APR-1999; 99US-0130891.
 XX PR 28-APR-1999; 99US-0131449.
 XX PR 30-APR-1999; 99US-0132048.
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 XX PR 07-MAY-1999; 99US-0132863.
 XX PR 11-MAY-1999; 99US-0134256.
 XX PR 14-MAY-1999; 99US-0134218.
 XX PR 14-MAY-1999; 99US-0134219.
 XX PR 14-MAY-1999; 99US-0134221.
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 XX PR 01-JUN-1999; 99US-0135629.
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 XX PR 24-MAY-1999; 99US-0137528.
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 XX PR 07-JUN-1999; 99US-0137724.
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 XX PR 10-JUN-1999; 99US-0138847.
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 XX PR 17-JUN-1999; 99US-0139457.
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 XX PR 18-JUN-1999; 99US-0139750.
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 XX PR 21-JUN-1999; 99US-0139817.

PR	22-JUN-1999;	99US-0139899.	PR	30-AUG-1999;	99US-0151303.
PR	23-JUN-1999;	99US-0140353.	PR	31-AUG-1999;	99US-0151438.
PR	23-JUN-1999;	99US-0140354.	PR	01-SEP-1999;	99US-0151930.
PR	24-JUN-1999;	99US-0140695.	PR	07-SEP-1999;	99US-0152363.
PR	28-JUN-1999;	99US-0140823.	PR	10-SEP-1999;	99US-0153070.
PR	29-JUN-1999;	99US-0140991.	PR	13-SEP-1999;	99US-0153758.
PR	30-JUN-1999;	99US-0141287.	PR	15-SEP-1999;	99US-0154018.
PR	01-JUL-1999;	99US-0141842.	PR	16-SEP-1999;	99US-0154039.
PR	01-JUL-1999;	99US-0142154.	PR	20-SEP-1999;	99US-0154779.
PR	02-JUL-1999;	99US-0142055.	PR	22-SEP-1999;	99US-0155139.
PR	06-JUL-1999;	99US-0142390.	PR	04-OCT-1999;	99US-0155486.
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PR	09-JUL-1999;	99US-0142977.	PR	07-OCT-1999;	99US-0156596.
PR	12-JUL-1999;	99US-0143542.	PR	08-OCT-1999;	99US-0157117.
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PR	19-JUL-1999;	99US-0144331.	PR	14-OCT-1999;	99US-0159330.
PR	19-JUL-1999;	99US-0144332.	PR	14-OCT-1999;	99US-0159331.
PR	19-JUL-1999;	99US-0144333.	PR	14-OCT-1999;	99US-015937.
PR	19-JUL-1999;	99US-0144334.	PR	14-OCT-1999;	99US-0159638.
PR	19-JUL-1999;	99US-0144335.	PR	18-OCT-1999;	99US-0159584.
PR	20-JUL-1999;	99US-0144332.	PR	21-OCT-1999;	99US-0160741.
PR	20-JUL-1999;	99US-0144632.	PR	21-OCT-1999;	99US-0160767.
PR	20-JUL-1999;	99US-0144633.	PR	21-OCT-1999;	99US-0160768.
PR	21-JUL-1999;	99US-0144884.	PR	21-OCT-1999;	99US-0160770.
PR	21-JUL-1999;	99US-0144814.	PR	21-OCT-1999;	99US-0160814.
PR	22-JUL-1999;	99US-0145086.	PR	21-OCT-1999;	99US-0161361.
PR	21-JUL-1999;	99US-0145088.	PR	22-OCT-1999;	99US-0160980.
PR	22-JUL-1999;	99US-0145085.	PR	22-OCT-1999;	99US-0160981.
PR	22-JUL-1999;	99US-0145087.	PR	22-OCT-1999;	99US-0161359.
PR	22-JUL-1999;	99US-0145089.	PR	26-OCT-1999;	99US-0161360.
PR	22-JUL-1999;	99US-0145192.	PR	26-OCT-1999;	99US-0161361.
PR	23-JUL-1999;	99US-0145088.	PR	25-OCT-1999;	99US-0161404.
PR	23-JUL-1999;	99US-0145145.	PR	25-OCT-1999;	99US-0161405.
PR	23-JUL-1999;	99US-0145218.	PR	25-OCT-1999;	99US-0161406.
PR	23-JUL-1999;	99US-0145224.	PR	26-OCT-1999;	99US-0161359.
PR	26-JUL-1999;	99US-0145276.	PR	26-OCT-1999;	99US-0161360.
PR	27-JUL-1999;	99US-0145913.	PR	28-OCT-1999;	99US-0161920.
PR	27-JUL-1999;	99US-0145918.	PR	28-OCT-1999;	99US-0161992.
PR	28-JUL-1999;	99US-0145919.	PR	28-OCT-1999;	99US-0161993.
PR	02-AUG-1999;	99US-0145951.	PR	29-OCT-1999;	99US-0162142.
PR	02-AUG-1999;	99US-0146386.	PR	29-OCT-1999;	99US-0162142.
PR	02-AUG-1999;	99US-0146388.	PR	32.68;	Score 598; DB 21; Length 210;
PR	03-AUG-1999;	99US-0147038.	Best Local Similarity	53.5%;	Pred. No. 2.4e-47;
PR	04-AUG-1999;	99US-0147204.	Matches 121; Conservative	35;	Mismatches 48; Indels 22; Gaps 3;
PR	04-AUG-1999;	99US-0147302.	QY	1 MGTILCSPKTDKTSEDDENAEELRYGLSAMQWRDSMEDAHKAIIIVDKNTSTSIFGIFDG	60
PR	05-AUG-1999;	99US-0147192.	Db	1 mgiy1stptktdkfsegedenhkiryglssmqwrasmedahailllddn--tsflgydg	58
PR	05-AUG-1999;	99US-0147260.	QY	61 HGGKLVAKECAKHLHQEVLKSEAYAKGDLKASLEYSFLRMDEMKGASGWKELQSLEETS	120
PR	06-AUG-1999;	99US-0147303.	Db	59 hggkvvsfkfcaky1hqqvlsdeayaqdvgtqlkaffrmdeammqgqrwrelavlgdk	118
PR	06-AUG-1999;	99US-0147416.	QY	121 SQLDKLNGN----NSSSNAREDDDESYSAVLTESNDSNLATKKHKSDFQGPYGSTA	175
PR	09-AUG-1999;	99US-0147493.	Db	119 nkfqmiegliwsprsgdsankpda-----waveeqphsdagpnsgsta	163
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PR	10-AUG-1999;	99US-0148171.	Db	164 cvavvrdkqfvanagsrcvisrkncaynlrsrdhkpdleakeri	209
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PR	16-AUG-1999;	99US-0149368.			
PR	17-AUG-1999;	99US-0149175.			
PR	18-AUG-1999;	99US-0149426.			
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PR	23-AUG-1999;	99US-0151065.			
PR	27-AUG-1999;	99US-0151066.			
PR	27-AUG-1999;	99US-0151080.			

XX AAG54775; 99US-0139462.
 XX 18-OCT-2000 (first entry) 99US-0139463.
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 69951.
 DE Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX OS Arabidopsis thaliana.
 XX EP1033405-A2. 99US-0139750.
 XX 06-SEP-2000. 99US-0139817.
 XX 25-FEB-2000; 2000EP-0301439. 99US-0139899.
 XX PR 25-FEB-1999; 99US-0121825. 99US-0139763.
 PR 05-MAR-1999; 99US-0123180. 99US-0139753.
 PR 09-MAR-1999; 99US-0123548. 99US-0139817.
 PR 23-MAR-1999; 99US-0125788. 99US-0139817.
 PR 25-MAR-1999; 99US-0126264. 99US-0139817.
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PR 25-AUG-1999; 99US-0150566.
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 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 32.0%; Score 588; DB 21; Length 293;
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Qy 223 SAGGFVHGGRVNGSLNLTRAIGDMEFKGRDLPDKQVVTCCPDVVEVDLGPDEFIVLA 282
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Qy 283 CDGIWDMSSQAVVDFVKSRLLPTKTLSSLCEELIDYCLSPTRQQEGCDNMSSIIIVQPK 342
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Qy 343 QSGVAASSSTD 353
 Db 269 kpnpsetepe 279